



DR WPI; 2002-500631/53.  
 DR N-PSDB; ABK88017.  
 XX  
 PT Novel fusion protein useful for inhibiting protease activity associated  
 PT with a disorder such as emphysema, asthma, comprises a first protease  
 PT inhibitor comprising alpha 1-antitrypsin and a second protease  
 PT inhibitor -  
 XX  
 PS Disclosure; Page 37; 134pp; English.  
 XX  
 CC This invention relates to a novel fusion protein comprising a first  
 CC protease inhibitor comprising an alpha 1-antitrypsin or its functionally  
 CC active portion and a second protease inhibitor or its functionally  
 CC active protein. The fusion proteins of the invention may act as an  
 CC inhibitor of protease activity. The fusion protein of the invention  
 CC is useful for inhibiting protease activity associated with a disorder  
 CC such as emphysema, asthma, chronic obstructive pulmonary disease,  
 CC cystic fibrosis, otitis media, otitis externa or HIV infection, or  
 CC for treating an individual suffering from or at risk for a disease or  
 CC disorder involving unwanted protease activity. The proteins are useful  
 CC for treating dermatological diseases such as atopic dermatitis, eczema  
 CC and psoriasis, in inflammatory responses to viral infection, and for  
 CC treating herpes infection, corneal or epidermal ulceration, chronic  
 CC non-healing wounds, sepsis, rheumatoid arthritis, periodontal disease,  
 CC tumour metastasis and tumour angiogenesis, gastric ulceration,  
 CC osteoporosis, Paget's disease, glomerulonephritis, scleroderma, malaria,  
 CC bacterial infection, Alzheimer's disease, hypertension and muscular  
 CC dystrophy. The present sequence represents the human tissue inhibitor  
 CC of metalloproteases used to create the fusion protein of the invention.  
 XX  
 SQ Sequence 184 AA;

Query Match 100.0%; Score 1009; DB 23; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-99;  
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCVPPHQTAFNCNSDLVIRAKFVGTPEVNQTTLYQRYEIKMTKMYKGFQALGDAADIRF 60  
 Db 1 CTCVPPHQTAFNCNSDLVIRAKFVGTPEVNQTTLYQRYEIKMTKMYKGFQALGDAADIRF 60  
 Qy 61 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCFVAPWNSLSLAQRGFTKTY 120  
 Db 61 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCFVAPWNSLSLAQRGFTKTY 120  
 Qy 121 TVGCECTVFPCLSPCKLQSGTHCLMTDQLQSGSEKGFQSRHLACLPRPGLCTWQSLR 180  
 Db 121 TVGCECTVFPCLSPCKLQSGTHCLMTDQLQSGSEKGFQSRHLACLPRPGLCTWQSLR 180  
 Qy 181 SQIA 184  
 Db 181 SQIA 184

RESULT 2  
 AAP60786  
 ID AAP60786 standard; Protein; 207 AA.  
 XX  
 AC AAP60786;  
 XX  
 DT 08-AUG-1991 (first entry)  
 XX  
 DE Sequence of tissue inhibitor of metalloproteinase (TIMP).  
 XX  
 KW Connective tissue; extracellular matrix.  
 XX  
 OS Homo sapiens.

XX Key Location/Qualifiers  
 FH Peptide 1..23  
 FT /label= signal  
 FT Protein 24..207  
 FT Modified-site 53..55  
 FT /label= potential N-glycosylation site

FT Modified-site 101..103  
 FT /label= as above  
 XX  
 PN GB2169295-A.  
 XX  
 PD 09-JUL-1986.  
 XX  
 PF 06-JAN-1986; 86GB-0000199.  
 XX  
 PR 01-NOV-1985; 85GB-0026951.  
 PR 07-JAN-1985; 85GB-0000341.  
 PR 06-JAN-1986; 86GB-0000199.  
 PR 07-JAN-1985; 85GB-0000341.  
 PR 05-OCT-1983; 83BE-0897924.  
 XX  
 PA (CELL-) CELLTech LTD.  
 XX  
 PI Harris TUR, Reynolds JJ, Docherty AJP, Murphy G;  
 XX  
 DR WPI; 1986-177873/28.  
 DR N-PSDB; AAN60538.  
 XX  
 PT Prodn. of metallo-proteinase inhibitors - by recombinant DNA  
 PT techniques  
 XX  
 PS Disclosure; Fig 3; 16pp; English.  
 XX  
 CC A gene with residues 64-684 of AAN60538 is claimed. AAN60538 was  
 CC isolated from human a foetal diploid lung cells (ATCC CELL153) cDNA  
 CC library using AAN60539.  
 XX  
 SQ Sequence 207 AA;

Query Match 100.0%; Score 1009; DB 7; Length 207;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-99;  
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCVPPHQTAFNCNSDLVIRAKFVGTPEVNQTTLYQRYEIKMTKMYKGFQALGDAADIRF 60  
 Db 24 CTCVPPHQTAFNCNSDLVIRAKFVGTPEVNQTTLYQRYEIKMTKMYKGFQALGDAADIRF 83  
 Qy 61 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCFVAPWNSLSLAQRGFTKTY 120  
 Db 84 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCFVAPWNSLSLAQRGFTKTY 143  
 Qy 121 TVGCECTVFPCLSPCKLQSGTHCLMTDQLQSGSEKGFQSRHLACLPRPGLCTWQSLR 180  
 Db 144 TVGCECTVFPCLSPCKLQSGTHCLMTDQLQSGSEKGFQSRHLACLPRPGLCTWQSLR 203  
 Qy 181 SQIA 184  
 Db 204 SQIA 207

RESULT 3  
 AAP60275  
 ID AAP60275 standard; Protein; 207 AA.  
 XX  
 AC AAP60275;  
 XX  
 DT 03-OCT-2002 (updated)  
 DT 08-AUG-1991 (first entry)  
 XX  
 DE Sequence of human natural inhibitor of collagenases (NIC).  
 XX  
 KW Metallo-proteinase inhibitor; wound healing; emphysema;  
 KW rheumatoid arthritis therapy; ulceration; tumour metastasis.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..23  
 FT /label= signal

FT Protein 24..207  
FT /note= "claimed"  
FT Modified-site 53..55  
FT /note= "potential glycosylation site"  
FT Modified-site 101..103  
FT /note= "potential glycosylation site"  
XX  
XX EPI89784-A.  
XX  
XX 06-AUG-1986.  
XX  
XX 16-JAN-1986; 86EP-0100482.  
XX  
XX 18-JAN-1985; 85US-0692808.  
XX  
XX (SEAR ) SEARLE G D & CO.  
XX  
XX Galloway WA, Clissold PM, McCullagh KG,  
XX  
XX MPI; 1986-205910/32.  
XX  
XX N-PSDB; AAN60277.  
XX  
PT New human natural inhibitor of collagenase - for treating e.g.  
PT rheumatoid arthritis or ulceration, and new DNA sequences coding  
PT for it  
XX  
XX PS Disclosure; Fig 2; 51pp; English.  
XX  
XX The patentors claim the AA SQ of human NIC, DNA sequences coding for  
XX NIC, and its RNA analogues and plasmids contg. this DNA. NIC  
XX inhibits the activity of metallo-proteinases, esp. of collagenase,  
XX proteoglycanase, gelatinase or a leucocyte, macrophage or tumour  
XX cell metallo-proteinase.  
XX  
XX (updated on 03-OCT-2002 to add missing OS field.)  
XX  
SQ Sequence 207 AA;  
Query Match 100.0%; Score 1009; DB 7; Length 207;  
Best Local Similarity 100.0%; Pred. No. 2.2e-99;  
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CTCVPPHQTAFCNSDLVIRAKFVGTPVNOITLYQRYEIKMTKMYKGFQALGDAADIRF 60  
DB 24 CTCVPPHQTAFCNSDLVIRAKFVGTPVNOITLYQRYEIKMTKMYKGFQALGDAADIRF 83  
QY 61 VYTPMESVCGYFHRSHNRSEFLIAGKLDGDLHITTCSPVAPWNSLSLAQRGFTKTY 120  
D 84 VYTPMESVCGYFHRSHNRSEFLIAGKLDGDLHITTCSPVAPWNSLSLAQRGFTKTY 143  
QY 121 TVGCECTVPFCLSIIPCKLQSGTHCLMTDQLQSGSEKGFQSRHLACLPRPGLCTWQSLR 180  
DB 144 TVGCECTVPFCLSIIPCKLQSGTHCLMTDQLQSGSEKGFQSRHLACLPRPGLCTWQSLR 203  
QY 181 SQIA 184  
DB 204 SQIA 207  
RESULT 4  
AAP60592  
ID AAP60592 standard; Protein; 207 AA.  
XX  
XX AAP60592;  
XX  
XX 13-AUG-1991 (first entry)  
XX  
XX Sequence of a human protein having erythroid potentiating  
DE activity (Epa).  
XX  
XX Erythroid precursor growth, anaemia therapy.  
XX  
XX Homo sapiens.  
XX

PN W08602100-A.  
XX  
XX 10-APR-1986.  
XX  
XX 01-OCT-1985; 85WO-5001900.  
XX  
XX 01-OCT-1984; 84US-0656590.  
XX  
XX (SANO ) SANDOZ LTD.  
PA (REGC ) REGENTS OF UNIV OF CALIF.  
XX  
XX Brown E, Clark S, Golde DW, Casson JC, Hewick R, Westbrook CA;  
XX  
XX MPI; 1986-106663/16.  
XX  
XX N-PSDB; AAN60494.  
XX  
XX Vectors contg. gene for protein having erythroid potentiating  
PT activity - used for producing protein to stimulate growth and  
PT formation of erythroid cells  
XX  
XX PS Disclosure; Fig 4; 59pp; English.  
XX  
XX The inventors claim human and gibbon EPA proteins (AAP60592, AAP60593)  
XX and cDNA that encodes EPA (AAN60494, AAN60495). The EPA protein has a  
XX biological activity of at least about 1,000,000 units per mg of  
XX protein and has an apparent molecular weight of about 28,000 daltons.  
XX  
SQ Sequence 207 AA;  
Query Match 100.0%; Score 1009; DB 7; Length 207;  
Best Local Similarity 100.0%; Pred. No. 2.2e-99;  
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CTCVPPHQTAFCNSDLVIRAKFVGTPVNOITLYQRYEIKMTKMYKGFQALGDAADIRF 60  
DB 24 CTCVPPHQTAFCNSDLVIRAKFVGTPVNOITLYQRYEIKMTKMYKGFQALGDAADIRF 83  
QY 61 VYTPMESVCGYFHRSHNRSEFLIAGKLDGDLHITTCSPVAPWNSLSLAQRGFTKTY 120  
DB 84 VYTPMESVCGYFHRSHNRSEFLIAGKLDGDLHITTCSPVAPWNSLSLAQRGFTKTY 143  
QY 121 TVGCECTVPFCLSIIPCKLQSGTHCLMTDQLQSGSEKGFQSRHLACLPRPGLCTWQSLR 180  
DB 144 TVGCECTVPFCLSIIPCKLQSGTHCLMTDQLQSGSEKGFQSRHLACLPRPGLCTWQSLR 203  
QY 181 SQIA 184  
DB 204 SQIA 207  
RESULT 5  
AAN60309  
ID AAN60309 standard; Protein; 207 AA.  
XX  
XX AAN60309;  
XX  
XX 29-JAN-1998 (first entry)  
XX  
XX Human TIMP-1.  
XX  
XX TIMP-3; human; antibody; TIMP-3-mediated disease; malignant tumour cell;  
XX cancer progression; TIMP-1.  
XX  
XX Homo sapiens.  
XX  
XX OS  
XX JP09235300-A.  
XX  
XX 09-SEP-1997.  
XX  
XX 29-FEB-1996; 96JP-0067484.  
XX  
XX 29-FEB-1996; 96JP-0067484.  
XX

PA (FUJII) FUJII PHARM IND CO LTD.  
 XX WPI; 1997-498341/46.  
 DR N-PSDB; AAT92631.  
 XX  
 XX Human TIMP-3 and anti-human TIMP-3 monoclonal antibodies - used in  
 PT diagnosis of TIMP-3 mediated diseases, especially the detection of  
 PT malignant tumour cells  
 XX  
 XX Example 12; Page 33-34; 37pp; Japanese.  
 PS  
 CC This sequence represents the human TIMP-1 protein. This sequence was  
 CC used to test the specificity of the monoclonal antibody (MAB) of the  
 CC invention. The MAB of the invention reacts specifically with human  
 CC TIMP-3 (see AAW30308), by specific recognition of the TIMP-3 fragments  
 CC represented by AAW30305-W30307. The MAB can be used in the study or  
 CC diagnosis of TIMP-3-mediated diseases, particularly for the detection of  
 CC malignant tumour cells, or the diagnosis of progressiveness of cancers.  
 CC They can also be used in establishing an immunoassay for TIMP-3 or in  
 CC purification of TIMP-3. The transformed cells can be used for producing  
 CC TIMP-3 or its equivalent proteins on a large scale. The immunoassay  
 CC method for TIMP-3 the MABs is simple, highly reproducible and highly  
 CC sensitive.  
 XX  
 XX Sequence 207 AA;  
 SQ

Query Match 100.0%; Score 1009; DB 18; Length 207;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-99;  
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVPPHPTAFNCNSDLVIRAKFVGTPEVNTTLQRYEIKMTKMYKGQALGDAADIRF 60  
 DB 24 CTCVPPHPTAFNCNSDLVIRAKFVGTPEVNTTLQRYEIKMTKMYKGQALGDAADIRF 83  
 QY 61 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCFVAPWNSLSLAORRGFTKTY 120  
 DB 84 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCFVAPWNSLSLAORRGFTKTY 143  
 QY 121 TVGCECTVFPCLSIIPCKLQSGTHCLWTDLQLGSEKGFQSRHLACLPREPGLCTWQSLR 180  
 DB 144 TVGCECTVFPCLSIIPCKLQSGTHCLWTDLQLGSEKGFQSRHLACLPREPGLCTWQSLR 203  
 QY 181 SQIA 184  
 DB 204 SQIA 207

RESULT 6  
 AAY08933  
 ID AAY08933 standard; Protein; 207 AA.  
 XX  
 AC AAY08933;  
 XX  
 DT 19-AUG-1999 (first entry)  
 XX  
 DE Human TIMP-1 protein.  
 XX  
 KW TIMP-4; tissue inhibitor of metalloprotease; human; antibody; diagnosis;  
 KW treatment; metastasis; neoplastic cell; angiogenesis; tumour; cervical;  
 KW uterine; pancreatic; colon; intestinal carcinoma; pregnancy; ulcer;  
 KW osteoarthritis; pulmonary emphysema; peridontal disease; corneal;  
 KW rheumatoid arthritis; diabetic ulcer; lesion; TIMP-4.  
 XX  
 OS Homo sapiens.  
 XX  
 XX US5914392-A.  
 PN  
 XX 22-JUN-1999.  
 PD  
 XX 07-JUL-1998; 98US-0111070.  
 PF  
 XX 18-JAN-1996; 96US-0588163.  
 PR  
 XX 27-JUN-1997; 97US-0884073.  
 PR

PR 07-JUL-1998; 98US-0111070.  
 XX  
 PA (INCY-) INCYTE PHARM INC.  
 XX  
 PI Hawkins PR, Murry LE;  
 XX  
 XX WPI; 1999-384187/32.  
 DR  
 XX Anti-tissue inhibitor metalloproteinase antibodies useful for  
 PT treating and diagnosing cancer  
 PT  
 XX Disclosure; Fig 4; 26pp; English.  
 PS  
 CC This invention describes a novel method for the production of antibodies  
 CC specific for the human tissue inhibitors of metalloproteinase 4, TIMP-4.  
 CC The anti-TIMP-4 antibodies may be used to treat, prevent or diagnose  
 CC metastasis of neoplastic cells, angiogenesis and growth tumours such as  
 CC cervical, uterine, pancreatic, colon or intestinal carcinomas, pregnancy,  
 CC osteoarthritis, pulmonary emphysema, peridontal disease, rheumatoid  
 CC arthritis, corneal or diabetic ulcers or ulcers and lesions caused by  
 CC microorganisms. This sequence represents TIMP-4 which is used to  
 CC describe the method of the invention.  
 XX  
 XX Sequence 207 AA;  
 SQ

Query Match 100.0%; Score 1009; DB 20; Length 207;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-99;  
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVPPHPTAFNCNSDLVIRAKFVGTPEVNTTLQRYEIKMTKMYKGQALGDAADIRF 60  
 DB 24 CTCVPPHPTAFNCNSDLVIRAKFVGTPEVNTTLQRYEIKMTKMYKGQALGDAADIRF 83  
 QY 61 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCFVAPWNSLSLAORRGFTKTY 120  
 DB 84 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCFVAPWNSLSLAORRGFTKTY 143  
 QY 121 TVGCECTVFPCLSIIPCKLQSGTHCLWTDLQLGSEKGFQSRHLACLPREPGLCTWQSLR 180  
 DB 144 TVGCECTVFPCLSIIPCKLQSGTHCLWTDLQLGSEKGFQSRHLACLPREPGLCTWQSLR 203  
 QY 181 SQIA 184  
 DB 204 SQIA 207

RESULT 7  
 AAB19073  
 ID AAB19073 standard; protein; 207 AA.  
 XX  
 AC AAB19073;  
 XX  
 DT 08-FEB-2001 (first entry)  
 XX  
 DE Inhibitor of tissue metalloproteinase designated TIMP-1.  
 XX  
 KW Tissue metalloproteinase inhibitor; TIMP; metalloproteinase; gelatinase;  
 KW metastasis; cancer.  
 XX  
 OS Unidentified.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..23  
 FT /note= "signal peptide"  
 FT Protein 24..207  
 FT /note= "mature protein"  
 XX  
 XX EP1041083-A1.  
 PN  
 XX 04-OCT-2000.  
 PD  
 XX 03-APR-2000; 2000EP-0107041.  
 PF  
 XX

PR 01-APR-1999; 99JP-0095142.  
 XX (ORIV ) ORIENTAL YEAST CO LTD.  
 XX Miyazaki K, Higashi S;  
 XX WPI: 2000-603816/58.  
 XX  
 PT New modified tissue inhibitor of metalloproteinases, useful for  
 PT manufacturing compositions for inhibiting metastasis of cancer and  
 PT vascularisation and for preventing or treating diseases associated with  
 PT these, e.g. brain tumor  
 XX  
 PS Disclosure; Page 12-13; 25pp; English.  
 XX  
 CC The present sequence represents an inhibitor of tissue metalloproteinase,  
 CC designated TIMP. The specification describes modified forms of TIMP,  
 CC where the amino-terminal alpha-amino group is modified with an electron  
 CC accepting group to substantially lose the ability to bind to a  
 CC metalloproteinase. Modified TIMP-2 prevents an accumulation of active  
 CC gelatinase. A on the cell surface, and can inhibit the activation of  
 CC precursor matrix metalloproteinases. The modified TIMP-2 and the  
 CC compositions comprising TIMP-2 are useful for inhibiting metastasis of  
 CC cancer and vascularisation. It is also used for treating diseases  
 CC associated with them. Specifically, these are useful for preventing or  
 CC treating metastasis of cancer of the stomach, colon, lung, head and  
 CC neck, brain tumor, breast, thyroid, prostate, ovary or pancreas, or  
 CC vascularisation or other conditions associated with these.  
 XX  
 SQ Sequence 207 AA;  
 Query Match 100.0%; Score 1009; DB 21; Length 207;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-99;  
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CTCVPHQQTAFNSDLVIRAKFVGTPEVNQTTLYQRYEIKMTKMYKGFQALGDAADIRF 60  
 DB 24 CTCVPHQQTAFNSDLVIRAKFVGTPEVNQTTLYQRYEIKMTKMYKGFQALGDAADIRF 83  
 QY 61 VYTPMSEVCGYFHRSHNRSEEFLLAGKLDGHLHTTCSFVAPWNSLSLQRRGFTTXY 120  
 DB 84 VYTPMSEVCGYFHRSHNRSEEFLLAGKLDGHLHTTCSFVAPWNSLSLQRRGFTTXY 143  
 QY 121 TVGSECTVFPCLSPCKLQSGTHCLMTDQLQSGSEKGFQSRHLACLPRPGLCTWQSLR 180  
 DB 144 TVGSECTVFPCLSPCKLQSGTHCLMTDQLQSGSEKGFQSRHLACLPRPGLCTWQSLR 203  
 QY 181 SQIA 184  
 DB 204 SQIA 207  
 RESULT 8  
 AAU99882  
 ID AAU99882 standard; Protein, 580 AA.  
 XX AAU99882;  
 XX  
 DT 07-OCT-2002 (first entry)  
 XX  
 DE TAP1 fusion protein.  
 XX  
 KM TAP1; Alzheimer's disease; tumour angiogenesis;  
 KM malaria; emphysema; asthma; chronic obstructive pulmonary disease;  
 KM cystic fibrosis; otitis media; otitis externa; HIV; psoriasis; eczema;  
 KM human immunodeficiency virus; atopic dermatitis; muscular dystrophy;  
 KM herpes; ulceration; sepsis; rheumatoid arthritis; periodontal disease;  
 KM tumour metastasis; osteoporosis; Paget's disease; scleroderma;  
 KM glomerulonephritis; hypertension.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX

FH Key Location/Qualifiers  
 FT Region 2..185  
 FT /note= "Human TIMP-1 amino acids 1-184"  
 FT Region 186  
 FT /note= "Linker methionine"  
 FT Region 187..580  
 FT /note= "Amino acids 1-394 of human AAT"  
 XX  
 XX WO200250287-A2.  
 XX  
 PD 27-JUN-2002.  
 XX  
 XX 18-DEC-2001; 2001WO-US49256.  
 XX  
 XX 18-DEC-2000; 2000US-256699P.  
 XX 20-NOV-2001; 2001US-331966P.  
 XX  
 XX (ARRI-) ARRIYA PHARM INC.  
 XX  
 XX Barr PJ, Gibson HL, Pemberton P;  
 XX  
 XX WPI: 2002-500631/53.  
 XX N-PSDB; ABK88023.  
 DR  
 PT Novel fusion protein useful for inhibiting protease activity associated  
 PT with a disorder such as emphysema, asthma, comprises a first protease  
 PT inhibitor comprising alpha 1-antitrypsin and a second protease  
 PT inhibitor -  
 XX  
 XX Example 1; Page 79-82; 134p; English.  
 PS  
 CC This invention relates to a novel fusion protein comprising a first  
 CC protease inhibitor comprising an alpha 1-antitrypsin or its functionally  
 CC active portion and a second protease inhibitor or its functionally  
 CC active portion. The fusion proteins of the invention may act as an  
 CC inhibitor of protease activity. The fusion protein of the invention  
 CC is useful for inhibiting protease activity associated with a disorder  
 CC such as emphysema, asthma, chronic obstructive pulmonary disease,  
 CC cystic fibrosis, otitis media, otitis externa or HIV infection, or  
 CC for treating an individual suffering from or at risk for a disease or  
 CC disorder involving unwanted protease activity. The proteins are useful  
 CC for treating dermatological diseases such as atopic dermatitis, eczema  
 CC and psoriasis, in inflammatory responses to viral infection, and for  
 CC treating herpes infection, corneal or epidermal ulceration, chronic  
 CC non-healing wounds, sepsis, rheumatoid arthritis, periodontal disease,  
 CC tumour metastasis and tumour angiogenesis, gastric ulceration,  
 CC osteoporosis, Paget's disease, glomerulonephritis, scleroderma, malaria,  
 CC bacterial infection, Alzheimer's disease, hypertension and muscular  
 CC dystrophy. The present sequence represents the TAP1 fusion protein of  
 CC the invention.  
 XX  
 SQ Sequence 580 AA;  
 Query Match 100.0%; Score 1009; DB 23; Length 580;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-99;  
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CTCVPHQQTAFNSDLVIRAKFVGTPEVNQTTLYQRYEIKMTKMYKGFQALGDAADIRF 60  
 DB 2 CTCVPHQQTAFNSDLVIRAKFVGTPEVNQTTLYQRYEIKMTKMYKGFQALGDAADIRF 61  
 QY 61 VYTPMSEVCGYFHRSHNRSEEFLLAGKLDGHLHTTCSFVAPWNSLSLQRRGFTTXY 120  
 DB 62 VYTPMSEVCGYFHRSHNRSEEFLLAGKLDGHLHTTCSFVAPWNSLSLQRRGFTTXY 121  
 QY 121 TVGSECTVFPCLSPCKLQSGTHCLMTDQLQSGSEKGFQSRHLACLPRPGLCTWQSLR 180  
 DB 122 TVGSECTVFPCLSPCKLQSGTHCLMTDQLQSGSEKGFQSRHLACLPRPGLCTWQSLR 181  
 QY 181 SQIA 184  
 DB 182 SQIA 185

RESULT 9  
 AAU99889 standard; Protein, 580 AA.  
 XX AAU99889;  
 AC AAU99889;  
 DT 07-OCT-2002 (first entry)  
 XX rTAP1 fusion protein.  
 DE rTAP1; Alzheimer's disease; tumour angiogenesis;  
 KW malaria; emphysema; asthma; chronic obstructive pulmonary disease;  
 KW cystic fibrosis; otitis media; otitis externa; HIV; psoriasis; eczema;  
 KW human immunodeficiency virus; atopic dermatitis; muscular dystrophy;  
 KW herpes; ulceration; sepsis; rheumatoid arthritis; periodontal disease;  
 KW tumour metastasis; osteoporosis; Paget's disease; scleroderma;  
 KW glomerulonephritis; hypertension.  
 XX Homo sapiens.  
 OS Synthetic.  
 OS  
 XX  
 FH Key Location/Qualifiers  
 FT Region 2..395  
 FT Region /note= "Human AAT amino acids 1-394"  
 FT Region 396  
 FT Region /note= "Linker methionine"  
 FT Region 397..580  
 FT Region /note= "Amino acids 1-184 of human TIMP-1"  
 XX  
 PN WO200250287-A2.  
 XX  
 PD 27-JUN-2002.  
 XX  
 PF 18-DEC-2001; 2001WO-US49256.  
 XX  
 XX 18-DEC-2000; 2000US-256699P.  
 PR 20-NOV-2001; 2001US-331966P.  
 XX  
 PA (ARRI-) ARRIVA PHARM INC.  
 XX  
 XX Barr PJ, Gibson HL, Pemberton P;  
 XX WPI; 2002-500631/53.  
 DR N-PSDB; ASK88026.  
 XX  
 PT Novel fusion protein useful for inhibiting protease activity associated  
 PT with a disorder such as emphysema, asthma, comprises a first protease  
 PT inhibitor comprising alpha 1-antitrypsin and a second protease  
 PT inhibitor -  
 XX  
 XX Example 3; Page 94; 134pp; English.  
 PS  
 XX This invention relates to a novel fusion protein comprising a first  
 CC protease inhibitor comprising an alpha-antitrypsin or its functionally  
 CC active portion and a second protease inhibitor or its functionally  
 CC active portion. The fusion proteins of the invention may act as an  
 CC inhibitor of protease activity. The fusion protein of the invention  
 CC is useful for inhibiting protease activity associated with a disorder  
 CC such as emphysema, asthma, chronic obstructive pulmonary disease,  
 CC cystic fibrosis, otitis media, otitis externa or HIV infection, or  
 CC for treating an individual suffering from or at risk for a disease or  
 CC disorder involving unwanted protease activity. The proteins are useful  
 CC for treating dermatological diseases such as atopic dermatitis, eczema  
 CC and psoriasis, in inflammatory responses to viral infection, and for  
 CC treating herpes infection, corneal or epidermal ulceration, chronic  
 CC non-healing wounds, sepsis, rheumatoid arthritis, periodontal disease,  
 CC tumour metastasis and tumour angiogenesis, gastric ulceration,  
 CC osteoporosis, Paget's disease, glomerulonephritis, scleroderma,  
 CC bacterial infection, Alzheimer's disease, hypertension and muscular  
 CC dystrophy. The present sequence represents the rTAP1 fusion protein of  
 CC the invention.

SQ Sequence 580 AA;  
 Query Match 100.0%; Score 1009; DB 23; Length 580;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-99;  
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CTCVPPHPQTAFNCNSDLVIRAKFVGTPEVNQTTLYQRYEIKMTKMYKGFQALGDAADIRF 60  
 DB 397 CTCVPPHPQTAFNCNSDLVIRAKFVGTPEVNQTTLYQRYEIKMTKMYKGFQALGDAADIRF 456  
 QY 61 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCFVAPWNSLSLAORRGFTKTY 120  
 DB 457 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCFVAPWNSLSLAORRGFTKTY 516  
 QY 121 TVGCECTVFPCLSIPIKQLSGTHCLMTDQLQSGEKGFQSRHLACLPREPGLCTWQSLR 180  
 DB 517 TVGCECTVFPCLSIPIKQLSGTHCLMTDQLQSGEKGFQSRHLACLPREPGLCTWQSLR 576  
 QY 181 SQIA 184  
 DB 577 SQIA 580  
 RESULT 10  
 AAP60593 standard; Protein, 207 AA.  
 ID AAP60593 standard; Protein, 207 AA.  
 XX AAP60593;  
 AC AAP60593;  
 XX 13-AUG-1991 (first entry)  
 DT  
 DE Sequence of a gibbon protein having erythroid potentiating  
 DE activity (EPA).  
 XX Erythroid precursor growth; anaemia therapy.  
 KW  
 XX Gibbon.  
 OS  
 XX WO8602100-A.  
 PN  
 PD 10-APR-1986.  
 XX  
 PF 01-OCT-1985; 85WO-5001900.  
 PR  
 PR 01-OCT-1984; 84US-0656590.  
 XX  
 PA (SANO ) SANDOZ LTD.  
 PA (REGC ) REGENTS OF UNIV OF CALIFO.  
 XX  
 PI Brown E, Clark S, Golde DW, Casson JC, Hewick R, Westbrook CA;  
 XX WPI; 1986-106663/16.  
 DR N-PSDB; AAN60495.  
 XX  
 PT Vectors contg. gene for protein having erythroid potentiating  
 PT activity - used for producing protein to stimulate growth and  
 PT formation of erythroid cells  
 XX  
 PS Disclosure; Fig 5; 59pp; English.  
 XX  
 CC The inventors claim human and gibbon EPA proteins (AAP60592, AAP60593)  
 CC and cDNA that encodes EPA (AAN60494, AAN60495). The EPA protein has a  
 CC biological activity of at least about 1,000,000 units per mg of  
 CC protein and has an apparent molecular weight of about 28,000 daltons.  
 XX  
 XX Sequence 207 AA;  
 Query Match 99.7%; Score 1006; DB 7; Length 207;  
 Best Local Similarity 99.5%; Pred. No. 4.6e-99;  
 Matches 183; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CTCVPPHPQTAFNCNSDLVIRAKFVGTPEVNQTTLYQRYEIKMTKMYKGFQALGDAADIRF 60

Db 24 CTCVPHQOTAFCSNDLYIRAKFVGTPEVNOTTLYQRYEIKMTKMYKGFQALGDAADIRF 83  
 QY 61 VYTPAMESVCGYFHRSHNRSEEFLLAGKLQDGLHITTCSEFVAPWNSLSLAQRGFTKTY 120  
 Db 84 VYTPAMESVCGYFHRSHNRSEEFLLAGKLQDGLHITTCSEFVAPWNSLSLAQRGFTKTY 143  
 QY 121 TVGCECTVFPCLSPCKLQSGTHCLMTDQLLQSGSEKGFQSRHLACLPREPGLCTWQSLR 180  
 Db 144 TVGCECTVFPCLSPCKLQSGTHCLMTDQLLQSGSEKGFQSRHLACLPREPGLCTWQSLR 203  
 QY 181 SQIA 184  
 Db 204 SQIA 207

## RESULT 11

AAG89171  
 ID AAG89171 standard; Protein; 207 AA.

XX AAG89171;  
 XX

DT 11-SEP-2001 (first entry)  
 XX

DE Human secreted protein; SEQ ID NO: 291.  
 XX

XX Human; secreted protein; gene therapy; vaccine; treatment; diagnosis;  
 KM GENSET.  
 XX

OS Homo sapiens.  
 XX

XX WO200142451-A2.  
 PN

PD 14-JUN-2001.  
 XX

PF 07-DEC-2000; 2000WO-IB01938.  
 XX

PR 08-DEC-1999; 99US-0169629.  
 XX

PR 06-MAR-2000; 2000US-0187470.  
 XX

XX (GENSET) GENSET.  
 PA

PI Dumas Mline Edwards J, Bougueleret L, Jobert S;  
 XX

DR WPI; 2001-367870/38.  
 XX

DR N-PSDB; AAH64774.  
 XX

PT Full length GENSET human nucleic acids encoding potentially secreted  
 XX proteins, useful in gene therapy and vaccination against a variety of  
 XX diseases, and for diagnosis of those diseases -

PS Claim 21; Page 825; 921pp; English.  
 XX

XX The invention relates to full length GENSET human nucleic acids encoding  
 CC potentially secreted proteins. The nucleic acids and the polypeptides  
 CC they encode may be used in the prevention, treatment and diagnosis of  
 CC diseases associated with inappropriate GENSET gene expression. For  
 CC example, they be used to treat disorders associated with decreased  
 CC GENSET gene expression by rectifying mutations or deletions in a  
 CC patient's genome that affect the activity of GENSET or by supplementing  
 CC the patient's own production of GENSET polypeptides. Conversely,  
 CC antisense nucleic acid molecules may be administered to down regulate  
 CC GENSET expression by binding with the cells' own genes and preventing  
 CC their expression. The sense and antisense nucleic acids may also be  
 CC used as DNA probes in diagnostic assays to detect and quantitate the  
 CC presence of similar nucleic acid sequences in samples, and hence to  
 CC determine which patients may be in need of restorative therapy.  
 CC The GENSET polypeptides may be used as antigens in the production of  
 CC antibodies and in assays to identify modulators (agonists and  
 CC antagonists) of GENSET polypeptide expression and activity. The  
 CC present sequence is a GENSET polypeptide of the invention.  
 XX

SQ Sequence 207 AA;  
 XX

Query Match 99.6%; Score 1005; DB 22; Length 207;  
 Best Local Similarity 99.5%; Pred. No. 5.8e-99;  
 Matches 183; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTCVPHQOTAFCSNDLYIRAKFVGTPEVNOTTLYQRYEIKMTKMYKGFQALGDAADIRF 60  
 Db 24 CTCVPHQOTAFCSNDLYIRAKFVGTPEVNOTTLYQRYEIKMTKMYKGFQALGDAADIRF 83  
 QY 61 VYTPAMESVCGYFHRSHNRSEEFLLAGKLQDGLHITTCSEFVAPWNSLSLAQRGFTKTY 120  
 Db 84 VYTPAMESVCGYFHRSHNRSEEFLLAGKLQDGLHITTCSEFVAPWNSLSLAQRGFTKTY 143  
 QY 121 TVGCECTVFPCLSPCKLQSGTHCLMTDQLLQSGSEKGFQSRHLACLPREPGLCTWQSLR 180  
 Db 144 TVGCECTVFPCLSPCKLQSGTHCLMTDQLLQSGSEKGFQSRHLACLPREPGLCTWQSLR 203  
 QY 181 SQIA 184  
 Db 204 SQIA 207

## RESULT 12

AAM93377  
 ID AAM93377 standard; Protein; 207 AA.

XX AAM93377;  
 XX

DT 06-NOV-2001 (first entry)  
 XX

DE Human polypeptide; SEQ ID NO: 2953.  
 XX

XX Human; full length cDNA; cDNA synthesis; oligo-capping.  
 KM

XX Homo sapiens.  
 OS

XX EP1130094-A2.  
 PN

PD 05-SEP-2001.  
 XX

PF 07-JUL-2000; 2000EP-0114089.  
 XX

PR 08-JUL-1999; 99JP-0194486.  
 XX

PR 11-JAN-2000; 2000JP-0118774.  
 XX

PR 02-MAY-2000; 2000JP-0183765.  
 XX

XX (HELI-) HELIX RES INST.  
 PA

PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;  
 XX Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
 XX

DR WPI; 2001-524255/58.  
 XX

DR N-PSDB; AAK94297.  
 XX

PT 830 Primers useful for synthesizing full length cDNA clones and their  
 XX use in genetic manipulation -

PS Claim 8; SEQ ID NO 2953; 1380bp + sequence listing; English.  
 XX  
 CC The invention relates to primers for synthesizing full length cDNA  
 CC clones. 830 cDNA molecules encoding a human protein have been  
 CC isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA  
 CC molecules have been determined. Primers for synthesizing the full length  
 CC cDNA are useful for clarifying the function of the protein encoded by  
 CC the cDNA. The full length clones were obtained by construction of full  
 CC length enriched cDNA libraries that were synthesised by the oligo-capping  
 CC method. The primers enable the production of the full length cDNA easily  
 CC without any special methods. The present sequence is a polypeptide  
 CC encoded by a full length human cDNA of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in CD-ROM format directly from EPO.  
 XX

SQ Sequence 207 AA;  
 XX

```
Query Match          99.5%; Score 1004; DB 22; Length 207;
Best Local Similarity 99.5%; Pred. No. 7.4e-99;
Matches 183; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTCVPHPTAFCSNDLVIRAKFVGTPVNTTLYQRYEIKMTKMYKGFQALGDAADIRF 60
DB 24 CTCVPHPTAFCSNDLVIRAKFVGTPVNTTLYQRYEIKMTKMYKGFQALGDAADIRF 83
QY 61 VYTPAMESVCGYFHRSHNRSEEFLLIAGKLDGLLHITTCFVAPWNLSLSLAQRGGFTKTY 120
DB 84 VYTPAMESVCGYFHRSHNRSEEFLLIAGKLDGLLHITTCFVAPWNLSLSLAQRGGFTKTY 143
QY 121 TVGCECTVFPCLSPCKLQSGTHCLWTDQLQSGSEKGFQSRHLACLPREPGLCTWQSUR 180
DB 144 TVGCECTVFPCLSPCKLQSGTHCLWTDQLQSGSEKGFQSRHLACLPREPGLCTWQSUR 203
QY 181 SQIA 184
DB 204 SQIA 207

RESULT 13
AAR65005
ID AAR65005 standard; Protein; 207 AA.
XX AC AAR65005;
XX DT 23-OCT-1995 (first entry)
XX DE Human tissue inhibitor of metalloproteinase (TIMP-1).
XX KW Tissue inhibitor of metalloproteinase; diagnostic; therapeutic;
XX KW prophylaxis.
XX OS Homo sapiens.
XX PN W09505478-A.
XX PD 23-FEB-1995.
XX PF 12-AUG-1994; 94WO-US09188.
XX PR 12-AUG-1993; 93US-0105263.
XX PR 13-DEC-1993; 93US-0167463.
XX PA (REGC ) UNIV CALIFORNIA.
XX PI Hawkes SP, Kishnani NS, Yang T;
XX DR WPI; 1995-098775/13.
XX PT New human tissue inhibitor of metalloproteinase-3 - used to
XX PT develop prods. for diagnosis, therapy or prophylaxis of
XX PT conditions with unwanted matrix metalloproteinase activity.
XX PS Disclosure; Fig 6A-B; 87pp; English.
XX CC The protein sequence of the human TIMP-1 is compared with those
XX CC from pig, cattle, rabbit and mouse TIMP-1, human, mouse and cattle
XX CC TIMP-2 and chicken (Ch) and mouse TIMP-3. A probe based on the
XX CC ChIMP-3 amino acid sequence (AAR65000) is used to isolate DNA
XX CC encoding human TIMP-3 from a human cDNA library. Human TIMP-3
XX CC can be used for the diagnosis, therapy or prophylaxis of
XX CC conditions characterized by excess or unwanted matrix
XX CC metalloproteinase activity, e.g. neoplasias, tumor metastasis,
XX CC inflammatory disorders such as rheumatoid arthritis, ulcerations,
XX CC reaction to infection, periodontal disease or osteoporosis. It can
XX CC also be used in drug screening/design.
XX SQ Sequence 207 AA;

Query Match          98.0%; Score 989; DB 16; Length 207;
Best Local Similarity 98.4%; Pred. No. 3e-97;

Matches 181; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTCVPHPTAFCSNDLVIRAKFVGTPVNTTLYQRYEIKMTKMYKGFQALGDAADIRF 60
DB 24 CTCVPHPTAFCSNDLVIRAKFVGTPVNTTLYQRYEIKMTKMYKGFQALGDAADIRF 83
QY 61 VYTPAMESVCGYFHRSHNRSEEFLLIAGKLDGLLHITTCFVAPWNLSLSLAQRGGFTKTY 120
DB 84 VYTPAMESVCGYFHRSHNRSEEFLLIAGKLDGLLHITTCFVAPWNLSLSLAQRGGFTKTY 143
QY 121 TVGCECTVFPCLSPCKLQSGTHCLWTDQLQSGSEKGFQSRHLACLPREPGLCTWQSUR 180
DB 144 TVGCECTVFPCLSPCKLQSGTHCLWTDQLQSGSEKGFQSRHLACLPREPGLCTWQSUR 203
QY 181 SQIA 184
DB 204 SQIA 207

RESULT 14
ABP42206
ID ABP42206 standard; Protein; 204 AA.
XX AC ABP42206;
XX DT 22-AUG-2002 (first entry)
XX DE Human ovarian antigen HCOQ079, SEQ ID NO:3338.
XX KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
XX KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
XX KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
XX KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
XX KW inflammatory condition; immune disorder; blood disorder;
XX KW cardiovascular disorder; respiratory disorder; neurological disorder;
XX KW gastrointestinal disorder; urinary system disorder; drug screening;
XX KW gene therapy; chromosome mapping; forensic analysis;
XX KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
XX KW antiinflammatory; gynaecological; reproductive.
XX OS Homo sapiens.
XX PN WO200200677-A1.
XX PD 03-JAN-2002.
XX PF 07-JUN-2001; 2001WO-US18569.
XX PR 07-JUN-2000; 2000US-209467P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Birse CE, Rosen CA;
XX DR WPI; 2002-147878/19.
XX DR N-PSDB; ABQ55283.
XX PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,
XX PT useful in the prevention, treatment and diagnosis of cancer (e.g.
XX PT ovarian cancer), immune disorders, cardiovascular disorders and
XX PT neurological diseases -
XX PS Claim 11; SEQ ID NO 3338; 2922pp; English.
XX CC The invention relates to 2175 novel human ovarian antigens (ABP41054-
XX CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
XX CC encompasses polypeptides 90% identical and polynucleotides 95% identical
XX CC to the sequences of the invention. The invention additionally relates to
XX CC recombinant vectors and host cells comprising human ovarian antigen
XX CC polynucleotides, antibodies against human ovarian antigens, and the use
XX CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
XX CC treating, prognosing or preventing various ovary and/or breast-related
XX CC disorders. Such conditions include ovarian cancer and breast cancer, and
```



CC metastatic tumours of ovarian or breast origin, reproductive system  
CC disorders (e.g., infertility, disorders of pregnancy, anovulation,  
CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhea), endocrine  
CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic  
CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and  
CC vaginitis), immune disorders (e.g., congenital and acquired  
CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),  
CC blood-related disorders (e.g., anaemia), cardiovascular disorders,  
CC respiratory disorders, neurological disorders, gastrointestinal disorders  
CC and urinary system disorders. Ovarian antigen polypeptides and  
CC polynucleotides may also be used in screening for compounds which  
CC modulate ovarian antigen expression or activity. The polynucleotides may  
CC further be used for gene therapy, chromosome mapping, in the  
CC identification of individuals and in forensic analysis, and the  
CC polypeptides may be used as food additives or to prepare antibodies  
CC useful in disease diagnosis, drug targeting and phenotyping. The present  
CC sequence represents a human ovarian antigen of the invention.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 204 AA:

Query Match 92.0%; Score 928; DB 23; Length 204;  
Best Local Similarity 99.4%; Pred. No. 9,4e-91;  
Matches 169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTCVPPHPQTAFCSNDVIRAKFVGTPEVNQTTLYORYEIKMTKMYKGFQALGDADIRF 60  
DB 22 CTCVPPHPQTAFCSNDVIRAKFVGTPEVNQTTLYORYEIKMTKMYKGFQALGDADIRF 81  
QY 61 VYTPMESVCGYFHRSHNRSEFLIAGKLDGDLHITTCSPFVAPWNSLSLAQRGFTKTY 120  
DB 82 VYTPMESVCGYFHRSHNRSEFLIAGKLDGDLHITTCSPFVAPWNSLSLAQRGFTKTY 141  
QY 121 TVGCECTVFPCLSIIPCKLQSGTHCLMTDQLLQSGSEKGFQSHLACLPRE 170  
DB 142 TVGCECTVFPCLSIIPCKLQSGTHCLMTDQLLQSGSEKGFQSHLACLPRE 191

RESULT 15

AAR65003 ID AAR65003 standard; Protein; 207 AA.

XX AAR65003;

DT 23-OCT-1995 (first entry)

XX Cattle tissue inhibitor of metalloproteinase (TIMP-1).

KM Tissue inhibitor of metalloproteinase; diagnostic; therapeutic;  
prophylaxis.

OS Bos primigenius taurus.

PN M09505478-A.

PD 23-FEB-1995.

PF 12-AUG-1994; 94WO-US09188.

PR 12-AUG-1993; 93US-0105263.

PR 13-DEC-1993; 93US-0167463.

PA (REGC ) UNIV CALIFORNIA.

PI Hawkes SP, Kishnani NS, Yang T;

WPI; 1995-098775/13.

PT New human tissue inhibitor of metallo:proteinase-3 - used to  
develop prods. for diagnosis, therapy or prophylaxis of  
PT conditions with unwanted matrix metallo:proteinase activity.

XX Disclosure: Fig 6A-B; 87pp; English.

XX The protein sequence of the cattle TIMP-1 is compared with those  
PS from pig, human, rabbit and mouse TIMP-1, human, mouse and cattle  
XX TIMP-2 and chicken (Ch) and mouse TIMP-3. A probe based on the  
CC ChIMP-3 amino acid sequence (AAR65000) is used to isolate DNA  
CC encoding human TIMP-3 from a human cDNA library. Human TIMP-3  
CC can be used for the diagnosis, therapy or prophylaxis of  
CC conditions characterized by excess or unwanted matrix  
CC metalloproteinase activity, e.g. neoplasias, tumor metastasis,  
CC inflammatory disorders such as rheumatoid arthritis, ulcerations,  
CC reaction to infection, periodontal disease or osteoporosis. It can  
CC also be used in drug screening/design.

XX Sequence 207 AA:

Query Match 88.5%; Score 893; DB 16; Length 207;  
Best Local Similarity 87.0%; Pred. No. 5,2e-87;  
Matches 160; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

QY 1 CTCVPPHPQTAFCSNDVIRAKFVGTPEVNQTTLYORYEIKMTKMYKGFQALGDADIRF 60  
DB 24 CTCVPPHPQTAFCSNDVIRAKFVGTAEVNETALYORYEIKMTKMYKGFQALRDADIRF 83  
QY 61 VYTPMESVCGYFHRSHNRSEFLIAGKLDGDLHITTCSPFVAPWNSLSLAQRGFTKTY 120  
DB 84 IYTPMESVCGYFHRSHNRSEFLIAGKLDGDLHITTCSPFVAPWNSLSLAQRGFTKTY 143  
QY 121 TVGCECTVFPCLSIIPCKLQSGTHCLMTDQLLQSGSEKGFQSHLACLPREGLCTWQSLR 180  
DB 144 AAGCECTVFPCLSIIPCKLQSGTHCLMTDQLLQSGSEKGFQSHLACLPREGLCTWQSLR 203  
QY 181 SQIA 184  
DB 204 AQMA 207

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Job time : 43.2414 secs

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

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Title: US-09-452-817-1

Perfect score: 1009  
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Scoring table: BLOSUM62  
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Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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6: /cgn2\_6/ptodata/1/1aa/backfilest.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	1009	100.0	207	US-08-588-163-5	Sequence 5, Appli
3	1009	100.0	207	US-09-111-070-5	Sequence 5, Appli
4	1009	100.0	207	US-08-849-764C-5	Sequence 5, Appli
5	1009	100.0	207	US-09-262-087-5	Sequence 5, Appli
6	1009	100.0	207	US-08-463-261B-11	Sequence 11, Appli
7	579	57.4	106	US-09-452-817-2	Sequence 2, Appli
8	377.5	37.4	211	US-08-588-163-4	Sequence 4, Appli
9	377.5	37.4	220	US-09-111-070-4	Sequence 4, Appli
10	377.5	37.4	220	US-08-588-163-3	Sequence 3, Appli
11	377.5	37.4	220	US-09-111-070-3	Sequence 3, Appli
12	372	36.9	210	US-08-849-764C-4	Sequence 4, Appli
13	372	36.9	210	US-09-262-087-4	Sequence 4, Appli
14	372	36.9	210	US-08-463-261B-10	Sequence 10, Appli
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16	369.5	36.6	218	US-09-262-087-3	Sequence 3, Appli
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18	351	34.8	224	US-08-588-163-2	Sequence 2, Appli
19	351	34.8	224	US-09-111-070-2	Sequence 2, Appli
20	351	34.8	224	US-08-849-764C-2	Sequence 2, Appli
21	351	34.8	224	US-09-262-087-2	Sequence 2, Appli
22	351	34.8	224	US-08-463-261B-2	Sequence 2, Appli
23	351	34.8	224	PCT-US93-14498A-2	Sequence 2, Appli
24	124	12.3	25	US-08-474-696A-2	Sequence 2, Appli
25	105	10.4	22	US-08-474-696A-5	Sequence 5, Appli
26	105	10.4	22	US-08-474-696A-6	Sequence 6, Appli
27	105	10.4	25	US-08-474-696A-4	Sequence 4, Appli

28	88.5	8.8	512	1	US-07-779-890-4	Sequence 4, Appli
29	88.5	8.8	512	1	US-07-779-890-4	Sequence 4, Appli
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31	88.5	8.8	512	2	US-08-675-507-4	Sequence 4, Appli
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35	77	7.6	16	2	US-08-480-190-134	Sequence 134, App
36	77	7.6	16	2	US-08-488-379-134	Sequence 134, App
37	77	7.6	16	5	PCT-US93-07545-134	Sequence 134, App
38	73	7.2	537	2	US-08-633-879C-2	Sequence 2, Appli
39	72.5	7.2	425	1	US-08-414-926A-15	Sequence 15, Appli
40	72.5	7.2	425	2	US-08-926-922-15	Sequence 15, Appli
41	72.5	7.2	425	3	US-09-253-682-15	Sequence 15, Appli
42	72.5	7.2	425	4	US-09-527-657-15	Sequence 15, Appli
43	72	7.1	15	2	US-08-480-190-135	Sequence 135, App
44	72	7.1	15	2	US-08-480-190-247	Sequence 247, App
45	72	7.1	15	2	US-08-488-379-135	Sequence 135, App

#### ALIGNMENTS

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RESULT 1
US-09-452-817-1
; Sequence 1, Application US/09452817
; Patent No. 6342374
; GENERAL INFORMATION:
; APPLICANT: Carmichael, David F
; APPLICANT: Anderson, David C
; APPLICANT: Stricklin, George P
; APPLICANT: Welgus, Howard G
; TITLE OF INVENTION: Human Collagenase Inhibitor, Recombinant Vector System
; TITLE OF INVENTION: For Using Same And Recombinant DNA Method For
; FILE REFERENCE: Serial No. 6342374 09/452,817
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US/09/452,817
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/050,739
; PRIOR FILING DATE: 1993-04-21
; PRIOR APPLICATION NUMBER: 07/853,018
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: 07/517,475
; PRIOR FILING DATE: 1990-05-01
; PRIOR APPLICATION NUMBER: 07/320,923
; PRIOR FILING DATE: 1989-03-08
; PRIOR APPLICATION NUMBER: 06/784,319
; PRIOR FILING DATE: 1985-10-04
; PRIOR APPLICATION NUMBER: 06/699,181
; PRIOR FILING DATE: 1985-02-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-452-817-1
Query Match      100.0%; Score 1009; DB 4; Length 184;
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Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CTCVPHQPTAFCSNLDVIRAKFVGTPEVNQTTLYORYEIMTKYKGFALGDAADIRF 60
DB 1 CTCVPHQPTAFCSNLDVIRAKFVGTPEVNQTTLYORYEIMTKYKGFALGDAADIRF 60
OY 61 VYTPMSEVCGYFPHSHRSEFLIAGKLDGLHITTCFVAPNNSISLAORGFTKTY 120
DB 61 VYTPMSEVCGYFPHSHRSEFLIAGKLDGLHITTCFVAPNNSISLAORGFTKTY 120
OY 121 TVGCECTVFPCLSIPTKLGSTGTHCLMTDQLQSGSEKGFQSRHLACLPRPGLCTWQSLR 180
```

Db 121 TVGCSECTVFPCLSPCKLQSGTHCLWTDQLQSGKGFQSRHLACLPRPGLCTWQSLR 180  
Qy 181 SQIA 184  
Db 181 SQIA 184

RESULT 2  
US-08-588-163-5  
; Sequence 5, Application US/08588163  
; Patent No. 5643752  
; GENERAL INFORMATION:  
; APPLICANT: Hawkins, Phillip R.  
; APPLICANT: Murry, Lynn E.  
; TITLE OF INVENTION: A NOVEL TISSUE INHIBITOR OF  
; TITLE OF INVENTION: METALLOPROTEINASES  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: US  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/588,163  
; FILING DATE: Herewith  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Luther, Barbara J.  
; REGISTRATION NUMBER: 33,954  
; REFERENCE/DOCKET NUMBER: PF-0053  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-852-0195  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 207 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; IMMEDIATE SOURCE:  
; LIBRARY: METALLOPROTEINASES  
; CLONE: TIMP-1  
US-08-588-163-5

Query Match 100.0%; Score 1009; DB 1; Length 207;  
Best Local Similarity 100.0%; Pred. No. 9e-117;  
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CTCVPPHPQTAFCSNDLVIRAKFVGTPEVNTTLYQRYEIKMTKMYKGFQALGDAADIRF 60  
Db 24 CTCVPPHPQTAFCSNDLVIRAKFVGTPEVNTTLYQRYEIKMTKMYKGFQALGDAADIRF 83  
Qy 61 VYTPAMESVCGYFHRSHNRSEFLIAGLQDGLLHITTCSFVAPWNSLSLAORRGFTKTY 120  
Db 84 VYTPAMESVCGYFHRSHNRSEFLIAGLQDGLLHITTCSFVAPWNSLSLAORRGFTKTY 143  
Qy 121 TVGCSECTVFPCLSPCKLQSGTHCLWTDQLQSGKGFQSRHLACLPRPGLCTWQSLR 180  
Db 144 TVGCSECTVFPCLSPCKLQSGTHCLWTDQLQSGKGFQSRHLACLPRPGLCTWQSLR 203

Qy 181 SQIA 184  
Db 204 SQIA 207  
RESULT 3  
US-09-111-070-5  
; Sequence 5, Application US/09111070  
; Patent No. 5914392  
; GENERAL INFORMATION:  
; APPLICANT: Hawkins, Phillip R.  
; APPLICANT: Murry, Lynn E.  
; TITLE OF INVENTION: A NOVEL TISSUE INHIBITOR OF  
; TITLE OF INVENTION: METALLOPROTEINASES  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: US  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/111,070  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/588,163  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Luther, Barbara J.  
; REGISTRATION NUMBER: 33,954  
; REFERENCE/DOCKET NUMBER: PF-0053  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-852-0195  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 207 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; IMMEDIATE SOURCE:  
; LIBRARY: METALLOPROTEINASES  
; CLONE: TIMP-1  
US-09-111-070-5

Query Match 100.0%; Score 1009; DB 2; Length 207;  
Best Local Similarity 100.0%; Pred. No. 9e-117;  
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CTCVPPHPQTAFCSNDLVIRAKFVGTPEVNTTLYQRYEIKMTKMYKGFQALGDAADIRF 60  
Db 24 CTCVPPHPQTAFCSNDLVIRAKFVGTPEVNTTLYQRYEIKMTKMYKGFQALGDAADIRF 83  
Qy 61 VYTPAMESVCGYFHRSHNRSEFLIAGLQDGLLHITTCSFVAPWNSLSLAORRGFTKTY 120  
Db 84 VYTPAMESVCGYFHRSHNRSEFLIAGLQDGLLHITTCSFVAPWNSLSLAORRGFTKTY 143  
Qy 121 TVGCSECTVFPCLSPCKLQSGTHCLWTDQLQSGKGFQSRHLACLPRPGLCTWQSLR 180  
Db 144 TVGCSECTVFPCLSPCKLQSGTHCLWTDQLQSGKGFQSRHLACLPRPGLCTWQSLR 203  
Qy 181 SQIA 184  
Db 204 SQIA 207

## RESULT 4

US-08-849-764C-5

; Sequence 5, Application US/08849764C  
; Patent No. 6300310

; GENERAL INFORMATION:

; APPLICANT: GREENE, JOHN M  
; ROSEN, CRAIG; TITLE OF INVENTION: HUMAN TISSUE INHIBITOR OF  
; METALLOPROTEINASE-4

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: HUMAN GENOME SCIENCES, INC.

; STREET: 9410 KEY WEST AVENUE

; CITY: ROCKVILLE

; STATE: MD

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/849,764C

; FILING DATE: 19-SEP-1997

; CLASSIFICATION: &lt;unknown&gt;

; ATTORNEY/AGENT INFORMATION:

; NAME: MICHELE M. WALES

; REGISTRATION NUMBER: 43, 975

; REFERENCE/DOCKET NUMBER: PF148US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 301-309-8504

; TELEFAX: 301-309-8439

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 207 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-08-849-764C-5

Query Match 100.0%; Score 1009; DB 4; Length 207;

Best Local Similarity 100.0%; Pred. No. 9e-117;

Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 1 CTCVPHPQTAFCSNDLVIRAKFVGTPPEVNOTTLVYQRYEIKMTKMYKGFQALGDAADIRF 60

Db 24 CTCVPHPQTAFCSNDLVIRAKFVGTPPEVNOTTLVYQRYEIKMTKMYKGFQALGDAADIRF 83

QY 61 VYTPMSEVCGYFHRSHRSEEFLLAGKLDGDLHITTCSEFVAPWNSLSLAORRGFTKTY 120

Db 84 VYTPMSEVCGYFHRSHRSEEFLLAGKLDGDLHITTCSEFVAPWNSLSLAORRGFTKTY 143

QY 121 TVGCECTVFPCLSIPTCKLQSGTHCLMTDQLLQSGSEKGFQSRHLACLPRPGLCTWQSLR 180

Db 144 TVGCECTVFPCLSIPTCKLQSGTHCLMTDQLLQSGSEKGFQSRHLACLPRPGLCTWQSLR 203

QY 181 SQIA 184

Db 204 SQIA 207

## RESULT 5

US-09-262-087-5

; Sequence 5, Application US/09262087

; Patent No. 6391853

; GENERAL INFORMATION:

; APPLICANT: GREENE, JOHN M

; ROSEN, CRAIG

## RESULT 6

US-08-463-261B-11

; Sequence 11, Application US/08463261B

; Patent No. 6448042

; GENERAL INFORMATION:

; APPLICANT: John M. Greene and Craig A. Rosen

; TITLE OF INVENTION: Human Tissue Inhibitor of Metalloproteinase-4

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: HUMAN GENOME SCIENCES, INC.

; STREET: 9410 KEY WEST AVENUE

; TITLE OF INVENTION: HUMAN TISSUE INHIBITOR OF

; METALLOPROTEINASE-4

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: HUMAN GENOME SCIENCES, INC.

; STREET: 9410 KEY WEST AVE

; CITY: ROCKVILLE

; STATE: MD

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/262,087

; FILING DATE: 04-MAR-1999

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/463,261

; FILING DATE: 05-JUN-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US94/14498

; FILING DATE: 13-FEB-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: A. ANDERS BROOKES

; REGISTRATION NUMBER: 36,373

; REFERENCE/DOCKET NUMBER: PF148PID1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 301-309-8504

; TELEFAX: 301-309-8439

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 207 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-09-262-087-5

Query Match 100.0%; Score 1009; DB 4; Length 207;

Best Local Similarity 100.0%; Pred. No. 9e-117;

Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 1 CTCVPHPQTAFCSNDLVIRAKFVGTPPEVNOTTLVYQRYEIKMTKMYKGFQALGDAADIRF 60

Db 24 CTCVPHPQTAFCSNDLVIRAKFVGTPPEVNOTTLVYQRYEIKMTKMYKGFQALGDAADIRF 83

QY 61 VYTPMSEVCGYFHRSHRSEEFLLAGKLDGDLHITTCSEFVAPWNSLSLAORRGFTKTY 120

Db 84 VYTPMSEVCGYFHRSHRSEEFLLAGKLDGDLHITTCSEFVAPWNSLSLAORRGFTKTY 143

QY 121 TVGCECTVFPCLSIPTCKLQSGTHCLMTDQLLQSGSEKGFQSRHLACLPRPGLCTWQSLR 180

Db 144 TVGCECTVFPCLSIPTCKLQSGTHCLMTDQLLQSGSEKGFQSRHLACLPRPGLCTWQSLR 203

QY 181 SQIA 184

Db 204 SQIA 207

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; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: 07/517,475
; PRIOR FILING DATE: 1990-05-01
; PRIOR APPLICATION NUMBER: 07/320,923
; PRIOR FILING DATE: 1989-03-08
; PRIOR APPLICATION NUMBER: 06/784,319
; PRIOR FILING DATE: 1985-10-04
; PRIOR APPLICATION NUMBER: 06/699,181
; PRIOR FILING DATE: 1985-02-05
; NUMBER OF SEQ. ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-452-817-2

Query Match          57.4%; Score 579; DB 4; Length 106;
Best Local Similarity 100.0%; Pred. NO. 5.4e-64;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 CTCVPHPQTAFNCSDLVIRAKFVGTPENVQNTLYORYEIKMTKMYKGFQALGDAADIRF 60
    |||
Db 1 CTCVPHPQTAFNCSDLVIRAKFVGTPENVQNTLYORYEIKMTKMYKGFQALGDAADIRF 60
    |||
QY 61 VYTPAMESVCGYFHRSHNRSEEFLLAGKLDQGLLHITTCSFVAPWN 106
    |||
Db 61 VYTPAMESVCGYFHRSHNRSEEFLLAGKLDQGLLHITTCSFVAPWN 106
    |||

RESULT 8
US-08-588-163-4
; Sequence 4, Application US/08588163
; Patent No. 5643752
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: A NOVEL TISSUE INHIBITOR OF
; TITLE OF INVENTION: METALLOPROTEINASES
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/588,163
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Luther, Barbara J.
; REGISTRATION NUMBER: 33,954
; REFERENCE/DOCKET NUMBER: PF-0053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-852-0195
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 211 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY: METALLOPROTEINASES  
CLONE: TIMP-3  
US-08-588-163-4

Query Match 37.4%; Score 377.5; DB 1; Length 211;

Best Local Similarity 40.8%; Pred. No. 1.3e-38;  
Matches 73; Conservative 33; Mismatches 62; Indels 11; Gaps 5;

QY 1 CTCVPHPTQACNSDLYIRAKVGTPEVNO--TTLYORYEIKMTKTKYKGFQALGDAD 57  
DB 24 CTCSPSHPDACNSDIVIRAKVGRKLVKEGPFGLV--YTIKQMKYRGFTKM---PH 78  
QY 58 IRFVVTTPAMESVCGYFHRSHNRSEFLIAGKLQDGLHITTCSFVAPMNSLSIAORRGT 117  
DB 79 VOYIHTEASESLICGL--KLEVNKRYQYLLTGRYVDGKMTTGLCNFYERWDQLTISQKGLN 136  
QY 118 KTYTVGCECTVPCLSLIPCKLQSGTHCLMTDQLLOGSEKGFQSHHACLPREPGLCTW 176  
DB 137 YRHHG-C-NCKIKSCYVLPFCVTSKNECLMTDMLSNFGYPGYQSHYACIRQKGYCSW 194

## RESULT 9

US-09-111-070-4  
Sequence 4, Application US/09111070  
Patent No. 5914392

GENERAL INFORMATION:

APPLICANT: Hawkins, Phillip R.

APPLICANT: Moriy, Lynn E.

TITLE OF INVENTION: A NOVEL TISSUE INHIBITOR OF

TITLE OF INVENTION: METALLOPROTEINASES

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: US

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/111.070

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/588,163

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Luther, Barbara J.

REGISTRATION NUMBER: 33,954

REFERENCE/DOCKET NUMBER: PF-0053

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555

TELEFAX: 415-852-0195

TELEX:

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 211 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

IMMEDIATE SOURCE:

LIBRARY: METALLOPROTEINASES

CLONE: TIMP-3

US-09-111-070-4

Query Match 37.4%; Score 377.5; DB 2; Length 211;

Best Local Similarity 40.8%; Pred. No. 1.3e-38;  
Matches 73; Conservative 33; Mismatches 62; Indels 11; Gaps 5;

QY 1 CTCVPHPTQACNSDLYIRAKVGTPEVNO--TTLYORYEIKMTKTKYKGFQALGDAD 57  
DB 24 CTCSPSHPDACNSDIVIRAKVGRKLVKEGPFGLV--YTIKQMKYRGFTKM---PH 78  
QY 58 IRFVVTTPAMESVCGYFHRSHNRSEFLIAGKLQDGLHITTCSFVAPMNSLSIAORRGT 117  
DB 79 VOYIHTEASESLICGL--KLEVNKRYQYLLTGRYVDGKMTTGLCNFYERWDQLTISQKGLN 136  
QY 118 KTYTVGCECTVPCLSLIPCKLQSGTHCLMTDQLLOGSEKGFQSHHACLPREPGLCTW 176  
DB 137 YRHHG-C-NCKIKSCYVLPFCVTSKNECLMTDMLSNFGYPGYQSHYACIRQKGYCSW 194

## RESULT 10

US-08-588-163-3  
Sequence 3, Application US/08588163  
Patent No. 5643752

GENERAL INFORMATION:

APPLICANT: Hawkins, Phillip R.

APPLICANT: Moriy, Lynn E.

TITLE OF INVENTION: A NOVEL TISSUE INHIBITOR OF

TITLE OF INVENTION: METALLOPROTEINASES

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: US

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/588,163

FILING DATE: Herewith

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Luther, Barbara J.

REGISTRATION NUMBER: 33,954

REFERENCE/DOCKET NUMBER: PF-0053

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555

TELEFAX: 415-852-0195

TELEX:

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 220 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

IMMEDIATE SOURCE:

LIBRARY: METALLOPROTEINASES

CLONE: TIMP-2

US-08-588-163-3

Query Match 37.4%; Score 377.5; DB 1; Length 220;  
Best Local Similarity 41.3%; Pred. No. 1.4e-38;  
Matches 76; Conservative 27; Mismatches 66; Indels 15; Gaps 6;

QY 1 CTCVPHPTQACNSDLYIRAKVGTPEVNO--TTLYO-----RYEIKMTKTKYKGFQALG 53  
DB 27 CSCSPVHPQOAFQADVIRAKVSEKEVDGNDIYGNPIKRIQYKIKWFK-----G 81

QY 54 DAADIRFVYTPAMESVCGYFHRSHNRSEBFLIAGKLO-DGLLHITTCSPVAPWNSLSLAQ 112  
DB 82 PKDIEFIYTPASSAVCG-VSLDVGKKEYLIAGKAEKWHITLDCDFIVPWTLSSTQ 140  
QY 113 RGFTKTYTVGCECTVFPCLSPCKLQSGTHCLWTDOLLOQSEKGFQSRHLACLPRPG 172  
DB 141 KASLNHRVQMG-C-ECKITRCMPICVYISSPDECLWMDWVTEKNGHQAQKFFACIKRSDG 199  
QY 173 LCTW 176  
DB 200 SCAW 203  
RESULT 11  
US-09-111-070-3  
; Sequence 3, Application US/09111070  
; Patent No. 5914392  
; GENERAL INFORMATION:  
; APPLICANT: Hawkins, Phillip R.  
; APPLICANT: Murry, Lynn E.  
; TITLE OF INVENTION: A NOVEL TISSUE INHIBITOR OF  
; TITLE OF INVENTION: METALLOPROTEINASES  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: US  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: Fast-Seq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/111,070  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/588,163  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Luther, Barbara J.  
; REGISTRATION NUMBER: 33,954  
; REFERENCE/DOCKET NUMBER: PF-0053  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-852-0195  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 220 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; IMMEDIATE SOURCE:  
; LIBRARY: METALLOPROTEINASES  
; CLONE: TIMP-2  
US-09-111-070-3  
Query Match 37.4%; Score 377.5; DB 2; Length 220;  
Best Local Similarity 41.3%; Pred. No. 1.4e-38;  
Matches 76; Conservative 27; Mismatches 66; Indels 15; Gaps 6;  
QY 1 CTCVPPHPQTAFNCNSDLVIRAKFVGTPEVNO--TTLYQ-----RVEIKMTKMYKGFQALG 53  
DB 27 CSCSPVHPQQAFCNADVVIRAKAVSEKVEYDSGNDIYGNPIKRIQYIEIKIMFK-----G 81  
QY 54 DAADIRFVYTPAMESVCGYFHRSHNRSEBFLIAGKLO-DGLLHITTCSPVAPWNSLSLAQ 112  
DB 82 PKDIEFIYTPASSAVCG-VSLDVGKKEYLIAGKAEKWHITLDCDFIVPWTLSSTQ 140

QY 113 RGFTKTYTVGCECTVFPCLSPCKLQSGTHCLWTDOLLOQSEKGFQSRHLACLPRPG 172  
DB 141 KASLNHRVQMG-C-ECKITRCMPICVYISSPDECLWMDWVTEKNGHQAQKFFACIKRSDG 199  
QY 173 LCTW 176  
DB 200 SCAW 203  
RESULT 12  
US-08-849-764C-4  
; Sequence 4, Application US/08849764C  
; Patent No. 6300310  
; GENERAL INFORMATION:  
; APPLICANT: GREENE, JOHN M  
; APPLICANT: ROSEN, CRAIG  
; TITLE OF INVENTION: HUMAN TISSUE INHIBITOR OF  
; TITLE OF INVENTION: METALLOPROTEINASE-4  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
; STREET: 9410 KEY WEST AVENUE  
; CITY: ROCKVILLE  
; STATE: MD  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/849,764C  
; FILING DATE: 19-Sep-1997  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MICHELE M. WALES  
; REGISTRATION NUMBER: 43,975  
; REFERENCE/DOCKET NUMBER: PF148US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 301-309-8504  
; TELEFAX: 301-309-8439  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 210 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-08-849-764C-4  
Query Match 36.9%; Score 372; DB 4; Length 210;  
Best Local Similarity 40.8%; Pred. No. 6.1e-38;  
Matches 73; Conservative 31; Mismatches 63; Indels 12; Gaps 5;  
QY 1 CTCVPPHPQTAFNCNSDLVIRAKFVGTPEVNO--TTLYQRYEIKMTKMYKGFQALGDAAD 57  
DB 24 CTCSPSPHPQDAFCNCDIVIRAKVVGKLVKREGPGTTLV--YTIKMKMYRGTQKPHV-- 79  
QY 58 IRFVYTPAMESVCGYFHRSHNRSEBFLIAGKLODGLLHITTCSPVAPWNSLSLAQRGFT 117  
DB 80 --YIHTASESLCGL--KLEVNKYQYLLTGRVYDGKMYTGLCNFVERWDQLTLSQRKGLN 135  
QY 118 KTYTVGCECTVFPCLSPCKLQSGTHCLWTDOLLOQSEKGFQSRHLACLPRPGCLCTW 176  
DB 136 YRYHLGC-NCKIKSCYLLPCFVTSKNECLWTDMLSNFGYQSGYQSKHVACIRKQKGYCSW 193  
RESULT 13  
US-09-262-087-4  
; Sequence 4, Application US/09262087



Patent No. 6391853  
GENERAL INFORMATION:  
APPLICANT: GREENE, JOHN M  
APPLICANT: ROSEN, CRAIG  
TITLE OF INVENTION: HUMAN TISSUE INHIBITOR OF  
METALLOPROTEINASE-4  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
STREET: 9410 KEY WEST AVE  
CITY: ROCKVILLE  
STATE: MD  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/262,087  
FILING DATE: 04-MAR-1999  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/463,261  
FILING DATE: 05-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/14498  
FILING DATE: 13-FEB-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: A. ANDERS BROOKES  
REGISTRATION NUMBER: 36,373  
REFERENCE/DOCKET NUMBER: PF148P1D1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-309-8504  
TELEFAX: 301-309-8439  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 210 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-262-087-4

Query Match 36.9%; Score 372; DB 4; Length 210;  
Best Local Similarity 40.8%; Pred. No. 6,1e-38;  
Matches 73; Conservative 31; Mismatches 63; Indels 12; Gaps 5;

QY 1 CTCVPHPOTAFCNDSLVIRAKFVGTPEVNO--TTLVQRYEIKMTKMYKGFQALGDAAD 57  
DB 24 CTCSPSHQDAFCNSDVIYIRAKVGVKLVKEGPGITLV--YTIKQMKYRGFTTKMPHY-- 79  
QY 58 IRFVYTPAMESVCGYFHRSHNRSEFLIAGKLQDGLHITTCSPFVAPWNSLSLAORGF 117  
DB 80 --YIHTASESLSGL--KLEVNKYQYLLTGRVYDGKMTGLCNFVERWDQTLTSQRKGLN 135  
QY 118 KTYVVGCECTVFPCLSTIPCKLQSGTGHCLMTDQLQSGSEKGFQSHLACLPRBPLCTW 176  
DB 136 YRHLGC-NCKIKSCYVLPFVTSKNELMTDMLSNFGYQSGHYACIRQKGYCSW 193

RESULT 14  
US-08-463-261B-10  
Sequence 10, Application US/08463261B  
Patent No. 6448042  
GENERAL INFORMATION:  
APPLICANT: John M. Greene and Craig A. Rosen  
TITLE OF INVENTION: Human Tissue Inhibitor of Metalloproteinase-4  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
STREET: 9410 KEY WEST AVENUE

CITY: ROCKVILLE  
STATE: MARYLAND  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 INCH DISKETTE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WORD PERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/463,261B  
FILING DATE: 05-JUN-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/14498  
FILING DATE: 13-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: KENLEY K. HOOVER  
REGISTRATION NUMBER: 40,302  
REFERENCE/DOCKET NUMBER: PF148P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-610-5790  
TELEFAX: 301-610-8439  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 210 AMINO ACIDS  
TYPE: AMINO ACID  
STRANDEDNESS:  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PROTEIN  
US-08-463-261B-10

Query Match 36.9%; Score 372; DB 4; Length 210;  
Best Local Similarity 40.8%; Pred. No. 6,1e-38;  
Matches 73; Conservative 31; Mismatches 63; Indels 12; Gaps 5;

QY 1 CTCVPHPOTAFCNDSLVIRAKFVGTPEVNO--TTLVQRYEIKMTKMYKGFQALGDAAD 57  
DB 24 CTCSPSHQDAFCNSDVIYIRAKVGVKLVKEGPGITLV--YTIKQMKYRGFTTKMPHY-- 79  
QY 58 IRFVYTPAMESVCGYFHRSHNRSEFLIAGKLQDGLHITTCSPFVAPWNSLSLAORGF 117  
DB 80 --YIHTASESLSGL--KLEVNKYQYLLTGRVYDGKMTGLCNFVERWDQTLTSQRKGLN 135  
QY 118 KTYVVGCECTVFPCLSTIPCKLQSGTGHCLMTDQLQSGSEKGFQSHLACLPRBPLCTW 176  
DB 136 YRHLGC-NCKIKSCYVLPFVTSKNELMTDMLSNFGYQSGHYACIRQKGYCSW 193

RESULT 15  
US-08-849-764C-3  
Sequence 3, Application US/08849764C  
Patent No. 6300310  
GENERAL INFORMATION:  
APPLICANT: GREENE, JOHN M  
APPLICANT: ROSEN, CRAIG  
TITLE OF INVENTION: HUMAN TISSUE INHIBITOR OF  
METALLOPROTEINASE-4  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
STREET: 9410 KEY WEST AVENUE  
CITY: ROCKVILLE  
STATE: MD  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/849,764C

```

; FILING DATE: 19-Sep-1997
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: MICHELE M. WALES
; REGISTRATION NUMBER: 43,975
; REFERENCE/DOCKET NUMBER: PF148US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-08-849-764C-3

Query Match      36.6%; Score 369.5; DB 4; Length 218;
Best Local Similarity 41.0%; Pred. No. 1.3e-37;
Matches 75; Conservative 28; Mismatches 65; Indels 15; Gaps 6;

Oy 1 CTCVPHPTAFCSNLDLVIRAKFVGTPVNO-----TTLYORYEIKMYKMGFOALGD 54
Db 27 CSCSPVHPQQAFCNADVVIRAKAVSEKVDGNDIYGNPIKRIYEIKI-KMEK----GP 80

Oy 55 AADIRFVYTPAMESVGYPHRSHNRSEFLIAGKLQ-DGLLHITTCSFVAPWNSLSLAOR 113
Db 81 EKDIETIYTPSSAVCG-VSLDVGGKKEYLIAGKAEKGGKMHITLCDFIVPMDTLSTQK 139

Oy 114 RGFTTYTVGCCECTVFPCLSPCKLQSGTHCLWTDQLQSGSEKGFQSRHLACLPRPGL 173
Db 140 KSLNHYQMGK-ECKITRCMPICVISSPDECLWMDWVTEKNGHQAKFFACIKRSDGS 198

Oy 174 CTW 176
Db 199 CAW 201
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Search completed: December 17, 2002, 15:06:33  
Job time : 15.5931 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: December 17, 2002, 15:04:31 ; Search time 18.4 Seconds

(without alignments)  
961.344 Million cell updates/sec

Title: US-09-452-817-1

Perfect score: 1009  
Sequence: 1 CTCVPPHPQTAFCNSDLVIR.....ACLPREPGLCTWGLRSQIA 184

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Sequenced: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1009	100.0	207	1	ZYHUEP metalloproteinase
2	1002	99.3	207	2	UC4303 matrix metalloprot
3	893	88.5	207	1	A35685 metalloproteinase
4	876	86.8	207	2	I46964 metalloproteinase
5	870	86.2	207	2	I47061 collagenase inhibi
6	817.5	81.0	206	1	A33350 metalloproteinase
7	761.5	75.5	205	1	A36106 metalloproteinase
8	742	73.5	217	1	UC2557 metalloproteinase
9	382.5	37.9	220	1	JH0683 metalloproteinase
10	382.5	37.8	220	2	I53415 metalloproteinase
11	381.5	37.8	212	1	A43429 metalloproteinase
12	379.5	37.6	196	1	S38624 metalloproteinase
13	378.5	37.6	220	1	S45683 metalloproteinase
14	377.5	37.4	211	1	S45317 metalloproteinase
15	377.5	37.4	220	1	A53128 metalloproteinase
16	372.5	37.0	211	1	A53532 metalloproteinase
17	372.5	36.9	211	2	UC4630 metalloproteinase
18	370.5	36.7	220	1	A35996 metalloproteinase
19	83	8.2	4307	2	T20721 hypothetical prote
20	77.5	7.7	944	2	S66870 DNA4 protein - yea
21	76.5	7.6	183	2	A32851 fixc protein homol
22	75.5	7.5	433	1	B65058 Probable Tail-like
23	75.5	7.5	530	2	F84488 mucin 2, intestina
24	75.5	7.5	1513	2	A54895 tumor necrosis fac
25	75	7.4	461	1	CGRTT1 metalloproteinase
26	74.5	7.4	50	2	I57129 histidine-tRNA lig
27	74.5	7.4	430	2	S73269 suppressor protein
28	74.5	7.4	444	2	S48966 protein K07C11.5
29	74	7.3	158	2	F89123

30	73.5	7.3	993	1	PIVXTA RNA 1 protein - to
31	73	7.2	537	2	I49135 prolyl 4-hydroxyla
32	73	7.2	555	2	D71444 probable thioester
33	72.5	7.2	611	2	A63926 hypothetical prote
34	71.5	7.1	533	2	T26860 hypothetical prote
35	71.5	7.1	581	2	T06825 ketol-acid reducto
36	71.5	7.1	1227	2	T23004 hypothetical prote
37	71.5	7.1	1339	2	UC4387 epidermal growth f
38	71	7.0	480	2	F82796 hypothetical prote
39	71	7.0	702	2	T16832 hypothetical prote
40	71	7.0	726	2	H96889 hypothetical prote
41	70.5	7.0	333	2	AF1582 molybdenum cofacto
42	70	6.9	266	2	S02510 nlfm protein - Kle
43	70	6.9	345	1	NBMS apolipoprotein H p
44	70	6.9	747	1	Gene 45 protein -
45	69.5	6.9	201	2	A47220 dermatopontin prec

## ALIGNMENTS

RESULT 1  
ZYHUEP  
Metalloproteinase tissue inhibitor 1 precursor [validated] - human  
N.Alternate names: erythroid potentiating activity (EPA); fibroblast collagenase inhibitor  
C.Species: Homo sapiens (man)  
C.Date: 28-May-1986 #sequence revision 28-May-1986 #text change 08-Dec-2000  
C.Accession: A93372; A93363; A23534; A20595; A35826; A48417; S20318; S15872; I52912; S664  
R.Docherty, A.U.P.; Lyons, A.; Smith, B.O.; Wright, E.M.; Stephens, P.E.; Harris, T.O.R.;  
Nature 318, 66-69, 1985  
A>Title: Sequence of human tissue inhibitor of metalloproteinases and its identity to ery  
A.Reference number: A93372; MUID:66040463; PMID:33903517  
A.Accession: A93372  
A.Molecule type: mRNA  
A.Residues: 1-207 <DOC>  
A.Cross-references: GB:X03124; NID:937182; PIDN:CAA26902.1; PID:937183  
R.Gascon, J.C.; Golde, D.W.; Kaufman, S.E.; Westbrook, C.A.; Hewick, R.M.; Kaufman, R.J.;  
Nature 315, 768-771, 1985  
A>Title: Molecular characterization and expression of the gene encoding human erythroid-1  
A.Reference number: A93363; MUID:85240567; PMID:3839290  
A.Accession: A93363  
A.Molecule type: mRNA  
A.Residues: 1-207 <GAS>  
R.Carmichael, D.F.; Sommer, A.; Thompson, R.C.; Anderson, D.C.; Smith, C.G.; Welgus, H.G.  
Proc. Natl. Acad. Sci. U.S.A. 83, 2407-2411, 1986  
A>Title: Primary structure and cDNA cloning of human fibroblast collagenase inhibitor.  
A.Reference number: A23534; MUID:86205964; PMID:3010309  
A.Accession: A23534  
A.Molecule type: mRNA  
A.Residues: 1-207 <CAR>  
A.Cross-references: GB:M12670; NID:g182482; PIDN:AAA52436.1; PID:g182483  
A.Note: parts of this sequence were confirmed by protein sequencing  
R.Stricklin, G.P.; Welgus, H.G.  
J. Biol. Chem. 258, 12252-12258, 1983  
A>Title: Human skin fibroblast collagenase inhibitor.  
A.Reference number: A20595; MUID:84032401; PMID:6313647  
A.Accession: A20595  
A.Molecule type: protein  
A.Residues: 24-44, 'L', 46 <STR>  
A.Note: six disulfide bonds are present  
R.Rapp, G.; Freudenstein, J.; Klaudiny, J.; Mucha, J.; Wempe, F.; Zimmer, M.; Scheit, K.I  
DNA Cell Biol. 9, 479-485, 1990  
A>Title: Characterization of three abundant mRNAs from human ovarian granulosa cells.  
A.Reference number: A35826; MUID:91035550; PMID:2171551  
A.Accession: A35826  
A.Molecule type: mRNA  
A.Residues: 1-207 <RAP>  
A.Cross-references: GB:M38188  
R.Van Ransst, M.; Norga, K.; Maasure, S.; Proost, P.; Vandekerckhove, F.; Auwerx, J.; Van I  
Cytokine 3, 231-239, 1991  
A>Title: The cytokine-protease connection: identification of a 96-kD RHP-1 gelatinase and  
A.Reference number: A48417; MUID:91355647; PMID:1653055

A:Accession: A48417  
A:Molecule type: protein  
A:Residues: 'X', 25, 'X', 27-35, 'X', 37-52 <VAN>  
A:Experimental source: monocytic cell line THP-1  
A:Note: sequence modified after extraction from NCBI backbone  
R:Osthues, A.; Knaeuper, V.; Oberhoff, R.; Reinke, H.; Tschesche, H.  
FEBS Lett. 296, 16-20, 1992  
A:Title: Isolation and characterization of tissue inhibitors of metalloproteinases (TIMP)  
A:Reference number: S20318; MUID:92111776; PMID:1730286  
A:Accession: S20318  
A:Molecule type: protein  
A:Residues: 'X', 25, 'X', 27-35, 'X', 37-38 <OST>  
A:Experimental source: rheumatoid synovial fluid  
R:Opdenakker, G.; Masure, S.; Proost, P.; Billiau, A.; van Damme, J.  
FEBS Lett. 284, 73-78, 1991  
A:Title: Natural human monocyte gelatinase and its inhibitor.  
A:Reference number: S15872; MUID:91285112; PMID:1647974  
A:Accession: S15872  
A:Molecule type: protein  
A:Residues: 'X', 25, 'X', 27-35, 'X', 37-42, 'X', 44, 'X', 46, 'X', 48-51 <FEB>  
A:Experimental source: peripheral blood monocytes  
R:Williamson, R.A.; Marston, F.A.O.; Angal, S.; Koklitis, P.; Panico, M.; Morris, H.R.;  
Biochem. J. 268, 267-274, 1990  
A:Title: Disulphide bond assignment in human tissue inhibitor of metalloproteinases (TIMP)  
A:Reference number: A38978; MUID:90303199; PMID:2163605  
A:Contents: annotation; disulfide bonds  
R:Opbroek, A.; Kenney, M.C.; Brown, D.  
Curr. Eye Res. 12, 877-883, 1993  
A:Title: Characterization of a human corneal metalloproteinase inhibitor (TIMP-1).  
A:Reference number: I52912; MUID:94123576; PMID:7507419  
A:Accession: I52912  
A:Status: translated from GB/EMBL/DBJ.  
A:Molecule type: mRNA  
A:Residues: 1-207 <RES>  
A:Cross-references: GB:S68252; NID:9545022; PIDN:AAD14009.1; PID:g4261709  
R:Triebel, S.; Blaszer, J.; Gote, T.; Pelz, G.; Schueren, E.; Schmitt, M.; Tschesche, H.  
Eur. J. Biochem. 231, 714-719, 1995  
A:Title: Evidence for the tissue inhibitor of metalloproteinases-1 (TIMP-1) in human pol  
A:Reference number: S66461; MUID:953377303; PMID:7649172  
A:Accession: S66461  
A:Molecule type: protein  
A:Residues: 24-38 <TRI>  
A:Experimental source: polymorphonuclear leukocytes  
C:Comment: This protein, found in a variety of body fluids, complexes with metalloprotei  
s-specific, stimulating the growth and differentiation of only human and murine erythro  
C:Comment: The remarkable heat stability of this protein may be due to disulfide bond fo  
C:Genetics:  
A:Gene: GDB:TIMP1; CLGI; TIMP  
A:Cross-references: GDB:I19615; OMIM:305370  
A:Map position: Xp11.3-Xp11.23  
C:Superfamily: metalloproteinase inhibitor  
C:Keywords: erythropoiesis; glycoprotein; metalloproteinase inhibitor; mitogen  
F:1-23/Domain: signal sequence #status predicted <SIG>  
F:24-207/Product: metalloproteinase inhibitor 1 #status experimental <MAT>  
F:24-93,26-122,36-147,150-197,155-160,168-189/Disulfide bonds: #status experimental  
F:53,101/Binding site: carbohydrate (Asn) (covalent) #status experimental  
Query Match 100.0%; Score 1009; DB 1; Length 207;  
Best Local Similarity 100.0%; Pred. No. 4.7e-94;  
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCVPPHPQTAFCSNLDLVIKAFVGTPEVNTTLYQRYEIKMTKMYKGFQALGDAADIRF 60  
Db 24 CTCVPPHPQTAFCSNLDLVIKAFVGTPEVNTTLYQRYEIKMTKMYKGFQALGDAADIRF 83  
Qy 61 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCFVAPWNSLSLAORRGFTKTY 120  
Db 84 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCFVAPWNSLSLAORRGFTKTY 143  
Qy 121 TVGCBECTVFPCLSIIPCKLQSGTHCLWTDQLQSGEKGFQSRHLACLPREPGLCTWQSLR 180  
Db 144 TVGCBECTVFPCLSIIPCKLQSGTHCLWTDQLQSGEKGFQSRHLACLPREPGLCTWQSLR 203

Qy 181 SQIA 184  
Db 204 SQIA 207  
RESULT 2  
JC4303  
matrix metalloproteinase-1 tissue inhibitor - baboon  
C:Species: Papio sp. (baboon)  
C:Date: 16-Nov-1995 #sequence\_revision 08-Feb-1996 #text\_change 16-Jul-1999  
A:Accession: JC4303  
R:Forough, R.; Nikkari, S.T.; Hasenstab, D.; Lea, H.; Clowes, A.W.  
Gene 163, 267-271, 1995  
A:Title: Cloning and characterization of a cDNA encoding the baboon tissue inhibitor of  
A:Reference number: JC4303; MUID:96011646; PMID:7590279  
A:Accession: JC4303  
A:Molecule type: mRNA  
A:Residues: 1-207 <FOR>  
A:Cross-references: GB:L37295; NID:g561545; PIDN:AAA99943.1; PID:g561546  
A:Experimental source: smooth muscle cell  
C:Comment: This protein, a member of the tissue inhibitor of matrix metalloproteinase f  
se and influences the proteinase activity. It has a role as a physiological molecule fo  
C:Genetics:  
A:Gene: timp-1  
C:Superfamily: metalloproteinase inhibitor  
C:Keywords: extracellular matrix; glycoprotein; metalloproteinase inhibitor  
F:53,101/Binding site: carbohydrate (Asn) (covalent) #status predicted  
Query Match 99.3%; Score 1002; DB 2; Length 207;  
Best Local Similarity 98.9%; Pred. No. 2.4e-93;  
Matches 182; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCVPPHPQTAFCSNLDLVIKAFVGTPEVNTTLYQRYEIKMTKMYKGFQALGDAADIRF 60  
Db 24 CTCVPPHPQTAFCSNLDLVIKAFVGTPEVNTTLYQRYEIKMTKMYKGFQALGDAADIRF 83  
Qy 61 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCFVAPWNSLSLAORRGFTKTY 120  
Db 84 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCFVAPWNSLSLAORRGFTKTY 143  
Qy 121 TVGCBECTVFPCLSIIPCKLQSGTHCLWTDQLQSGEKGFQSRHLACLPREPGLCTWQSLR 180  
Db 144 TVGCBECTVFPCLSIIPCKLQSGTHCLWTDQLQSGEKGFQSRHLACLPREPGLCTWQSLR 203  
Qy 181 SQIA 184  
Db 204 TRIA 207  
RESULT 3  
A35685  
metalloproteinase inhibitor 1 precursor - bovine  
N:Alternate names: cartilage-derived neovascularization inhibitor; TIMP-1; tissue inhibi  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 21-Sep-1990 #sequence\_revision 12-Apr-1996 #text\_change 18-Jun-1999  
C:Accession: A35685; B34468; B29712; A34833; I46979  
R:Freudenstein, J.; Wagner, S.; Luck, R.M.; Einspanier, R.; Scheit, K.H.  
Biochem. Biophys. Res. Commun. 171, 250-256, 1990  
A:Title: mRNA of bovine tissue inhibitor of metalloproteinase: sequence and expression  
A:Reference number: A35685; MUID:90365711; PMID:2393392  
A:Accession: A35685  
A:Molecule type: mRNA  
A:Residues: 1-207 <FRE>  
A:Cross-references: GB:M60073; NID:g163760; PIDN:AAA30784.1; PID:g163761  
R:De Clerck, Y.A.; Yeon, T.D.; Ratzkin, B.J.; Lu, H.S.; Langley, K.E.  
J. Biol. Chem. 264, 17445-17453, 1989  
A:Title: Purification and characterization of two related but distinct metalloproteinai  
A:Reference number: A34468; MUID:90008914; PMID:2551903  
A:Accession: B34468  
A:Molecule type: protein  
A:Residues: 24-52, 'X', 54-57, 'LY', 60-61, 'L', 63-65, 'L', 67-68, 'P' <DEC>

A:Experimental source: culture medium of aortic endothelial cells  
R:Kaczorek, M.; Honore, N.; Ribes, V.; Dehoux, P.; Cornet, P.; Cartwright, T.; Streeck, Bio/Technology 5, 595-598, 1987  
A:Title: Molecular cloning and synthesis of biologically active human tissue inhibitor c  
A:Reference number: A29712  
A:Accession: B29712  
A:Molecule type: protein  
A:Residues: 24-37 <KAC>  
A:Experimental source: culture medium of fibroblastic BC 21 cells  
R:Moses, M.A.; Sudhalter, J.; Langer, R.  
Science 248, 1408-1410, 1990  
A:Title: Identification of an inhibitor of neovascularization from cartilage.  
A:Reference number: A34833; MUID:90288433; PMID:1694043  
A:Accession: A34833  
A:Molecule type: protein  
A:Residues: 24-51 <MOS>  
A:Experimental source: cartilage  
R:Ch, T.; Kobayashi, K.; Yamashita, S.; Kikuchi, M.; Sendai, Y.; Hoshi, H.  
Reprod. 50, 835-844, 1994  
A:Title: Tissue inhibitor of metalloproteinases (TIMP-1) produced by granulosa and oviduct  
A:Reference number: 146979; MUID:94257757; PMID:8199264  
A:Accession: 146979  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-207 <SAT>  
A:Cross-references: GB:570841; NID:g546973; PID:AA30892.1; PID:g546974  
C:Function:  
A:Description: regulation of extracellular matrix remodeling by inhibition of matrix met  
possibly controlling their activation; TIMP-1 and TIMP-2 possess erythroid potentiating  
A>Note: transcription induced by cytokines, tumor promoters, and anti-inflammatory agent  
A>Note: TIMP-1 and TIMP-3 have distinct but overlapping tissue-specific expression patte  
C:Superfamily: metalloproteinase inhibitor  
C:Keywords: erythropoiesis; extracellular matrix; glycoprotein; metalloproteinase inhibi  
F:1-23/Domain: signal sequence #status predicted <Sig>  
F:24-207/Product: metalloproteinase inhibitor 1 #status experimental <MAT>  
F:24-93,26-122,36-147,150-157,155-160,168-189/Disulfide bonds: #status predicted  
F:53,101/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 88.5%; Score 893; DB 1; Length 207;  
Best Local Similarity 87.0%; Pred. No. 2,3e-82;  
Matches 160; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

Q 1 CTCVPHPQTAFNCSDLVIRAKFVGTPEVNOTTLVYRVEIKMTKMYKGFQALGDAADIRF 60  
Db 24 CTCVPHPQTAFNCSDLVIRAKFVGTAEVNETALVYRVEIKMTKMYKGFQALGDAADIRF 83  
Q 61 VYTPAMSVCGYFHRSHNRSEEFLLAGLQDGLHITTCSPVAPWNSLSLAQRGFTKTY 120  
Db 84 IYTPAMSVCGYFHRSHNRSEEFLLAGLQDGLHITTCSPVAPWNSLSLAQRGFTKTY 143  
Q 121 TVGCECTVPFCLSPCKLQSGTHCLMTDQLLQSGEKFGQSRHLACLPRPGLCTWOSLR 180  
Db 144 AAGEECTVPFCLSPCKLQSGTHCLMTDQLLQSGDKFGQSRHLACLPRPGLCTWOSLR 203  
Q 181 SQIA 184  
Db 204 AQMA 207

RESULT 4  
146964  
metalloproteinase tissue inhibitor 1 precursor [similarity] - sheep  
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 19-Jan-2001  
C:Accession: 146964  
R:Smith, G.W.; Goetz, T.L.; Anthony, R.V.; Smith, M.F.  
Endocrinology 134, 344-352, 1994  
A:Title: Molecular cloning of an ovine ovarian tissue inhibitor of metalloproteinases: c  
eal tissue.  
A:Reference number: 146964; MUID:94102210; PMID:8275949  
A:Accession: 146964  
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA  
A:Residues: 1-207 <SMI>  
A:Cross-references: GB:567450; NID:g456989; PID:AA29472.1; PID:g456990  
C:Superfamily: metalloproteinase inhibitor

Query Match 86.8%; Score 876; DB 2; Length 207;  
Best Local Similarity 86.7%; Pred. No. 1.2e-80;  
Matches 156; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

Q 1 CTCVPHPQTAFNCSDLVIRAKFVGTPEVNOTTLVYRVEIKMTKMYKGFQALGDAADIRF 60  
Db 24 CTCVPHPQTAFNCSEVIVIRAKFVGTAEVNETALVYRVEIKMTKMYKGFQALGDAADIRF 83  
Q 61 VYTPAMSVCGYFHRSHNRSEEFLLAGLQDGLHITTCSPVAPWNSLSLAQRGFTKTY 120  
Db 84 IYTPAMSVCGYFHRSHNRSEEFLLAGLQDGLHITTCSPVAPWNSLSLAQRGFTKTY 143  
Q 121 TVGCECTVPFCLSPCKLQSGTHCLMTDQLLQSGEKFGQSRHLACLPRPGLCTWOSLR 180  
Db 144 AAGEECTVPFCLSPCKLQSGTHCLMTDQLLQSGDKFGQSRHLACLPRPGLCTWOSLR 203  
Q 181 SQIA 184  
Db 204 PRVA 207

RESULT 5  
147061  
collagenase inhibitor - pig  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 04-Sep-1997 #sequence\_revision 04-Sep-1997 #text\_change 16-Jul-1999  
C:Accession: 147061  
R:Tanaka, T.; Andoh, N.; Takeya, T.; Sato, E.  
Mol. Cell. Endocrinol. 83, 65-71, 1992  
A:Title: Differential screening of ovarian cDNA libraries detected the expression of the  
A:Reference number: 147061; MUID:92201478; PMID:1312961  
A:Accession: 147061  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-207 <TMN>  
A:Cross-references: GB:596211; NID:g247729; PID:AA21865.1; PID:g247730  
C:Superfamily: metalloproteinase inhibitor

Query Match 86.2%; Score 870; DB 2; Length 207;  
Best Local Similarity 83.7%; Pred. No. 4.7e-80;  
Matches 154; Conservative 13; Mismatches 17; Indels 0; Gaps 0;

Q 1 CTCVPHPQTAFNCSDLVIRAKFVGTPEVNOTTLVYRVEIKMTKMYKGFQALGDAADIRF 60  
Db 24 CTCVPHPQTAFNCSDLVIRAKFVGTAEVNETALVYRVEIKMTKMYKGFQALGDAADIRF 83  
Q 61 VYTPAMSVCGYFHRSHNRSEEFLLAGLQDGLHITTCSPVAPWNSLSLAQRGFTKTY 120  
Db 84 IYTPAMSVCGYFHRSHNRSEEFLLAGLQDGLHITTCSPVAPWNSLSLAQRGFTKTY 143  
Q 121 TVGCECTVPFCLSPCKLQSGTHCLMTDQLLQSGEKFGQSRHLACLPRPGLCTWOSLR 180  
Db 144 AAGEECTVPFCLSPCKLQSGTHCLMTDQLLQSGDKFGQSRHLACLPRPGLCTWOSLR 203  
Q 181 SQIA 184  
Db 204 PRVA 207

RESULT 6  
A33350  
metalloproteinase inhibitor 1 precursor - rabbit  
N:Alternate names: TIMP-1; tissue inhibitor of metalloproteinases 1  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 30-Jun-1992 #sequence\_revision 12-Apr-1996 #text\_change 18-Jun-1999  
C:Accession: A33350; A30864  
R:Horowitz, S.; Dafni, N.; Shapiro, D.L.; Holm, B.A.; Notter, R.H.; Quible, D.J.  
J. Biol. Chem. 266, 7092-7095, 1991  
A:Title: Hypertoxic exposure alters gene expression in the lung. Induction of the tissue i  
A:Reference number: A33350; MUID:89214135; PMID:2708356  
A:Accession: A33350  
A:Molecule type: mRNA

A;Residues: 168-193,'L','L',195-205 <SKU>  
A;Cross-references: GB:I00755; GB:J00425; NID:g5l554; PIDN:CAA24132.1; PID:g817965  
A;Note: authors thought this clone represented a form of interferon beta  
C;Genetics:  
A;Gene: Timp  
A;Map position: X  
A;Introns: 41/3; 68/3; 110/3; 152/3  
C;Function:  
A;Description: regulation of extracellular matrix remodeling by inhibition of matrix metalloproteinase  
possibly controlling their activation; TIMP-1 and TIMP-2 possess erythroid potentiating activity  
A;Note: transfection induced by cytokines, tumor promoters, and anti-inflammatory agents  
A;Note: TIMP-1 and TIMP-3 have distinct but overlapping tissue-specific expression pattern  
C;Superfamily: metalloproteinase inhibitor  
F;Keywords: erythropoiesis; extracellular matrix; glycoprotein; metalloproteinase inhibitor  
F;1-24/Domain: signal sequence #status predicted <SIG>  
F;25-205/Product: metalloproteinase inhibitor 1 #status predicted <MAT>  
F;25-94, 27-123, 37-148, 151-197, 156-161, 169-189/Diulfide bonds: #status predicted  
F;54,102/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 75.5%; Score 761.5; DB 1; Length 205;  
Best Local Similarity 73.7%; Pred. No. 3.9e-69;  
Matches 132; Conservative 25; Mismatches 21; Indels 1; Gaps 1;

QY 1 CTCVPHPTAFNCNSDLIVIRAKFTGTVENVQTLYQRYEIKMTMYKGFQALGDADIRF 60  
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 25 CSCAPHPPTAFNCNSDLIVIRAKFTGSPSEINETTLTYQRYIKMTKMLKGFKAVGAADIRY 84  
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
QY 61 VYTPAMESVCGYHRSHNRSEEFILACKLDGLLIHTTCSPVAPWNSISLAORSGFTKTY 120  
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 85 AYTPVMESLCGYAHKSQNRSSEEFILTRLRNLGNLHISACSLVPWRITLSPAQQRAFSKYT 144  
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
QY 121 TVGCCTVFPPCLSIPOCKLOSTGHCHLTDLQLLOGSEKGFOSRHIACLPREPGCLTWQSL 179  
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 145 SAGCGVTVPCLSIPOCKLESSTHCLWTQDVLVGSE-DYQSRHFACLPRLNPLCTWRSL 202  
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 8  
JC2557  
Metalloproteinase inhibitor 1 precursor - rat  
N;Alternate names: TIMP-1  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C;Accession: JC2557; B39120; S20326  
R;Okada, A.; Garnier, J.M.; Vicaire, S.; Bassett, P.  
Gene 147, 301-302, 1994  
A;Title: Cloning of the cDNA encoding rat tissue inhibitor of metalloproteinase 1 (TIMP-1)  
A;Reference number: JC2557; MUID:95011636; PMID:7926820  
A;Accession: JC2557  
A>Status: preliminary  
A:Molecule type: mRNA  
A;Residues: 1-217 <OKA>  
A;Cross-references: EMBL:U06179; NID:g468057; PIDN:AA85780.1; PID:g468058  
R;Olson Jr., J.A.; Shiverick, K.T.; Ogilvie, S.; Buhi, W.C.; Raizada, M.K.  
Proc. Natl. Acad. Sci. U.S.A. 88, 1928-1932, 1991  
A;Title: Angiotensin II induces secretion of plasminogen activator inhibitor 1 and a tissue inhibitor of metalloproteinase  
A;Reference number: A39120; MUID:91156719; PMID:2000398  
A;Accession: B39120  
A>Status: preliminary  
A:Molecule type: protein  
A;Residues: 24-36,'B','38','B',40-42,'X',44 <OLS>  
R;Roswit, W.T.; McCourt, D.W.; Partridge, N.C.; Jeffrey, J.J.  
Arch. Biochem. Biophys. 292, 402-410, 1992  
A;Title: Purification and sequence analysis of two rat tissue inhibitors of metalloprotease  
A;Reference number: S20325; MUID:92117648; PMID:1309971  
A;Accession: S20326  
A:Molecule type: protein  
A;Residues: 24-45 <ROS>  
C;Function:  
A;Description: regulation of extracellular matrix remodeling by inhibition of matrix metalloproteinase  
possibly controlling their activation; TIMP-1 and TIMP-2 possess erythroid potentiating activity  
A;Note: transfection induced by cytokines, tumor promoters, and anti-inflammatory agents  
A;Note: TIMP-1 and TIMP-3 have distinct but overlapping tissue-specific expression pattern  
C;Superfamily: metalloproteinase inhibitor

Matches	77;	Conservative	27;	Mismatches	65;	Indels	15;	Gaps	6;
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A/Cross-references: GB:M94531; NID:q211901; PIDN:AAA48813.1; PID:q211902

A:Experimental source: ten-day old embryo cdna library  
A:Note: sequence extracted from NCBI backbone (NCBIN:111960, NCBI:P:111961)  
J:Staskus, P.W.; Mastarz, F.R.; Pallanck, L.J.; Hawkes, S.P.  
J. Biol. Chem. 266, 449-454, 1991  
A:Title: The 21-kDa protein is a transformation-sensitive metalloproteinase inhibitor of  
A:Reference number: A39043; MUID:91093162; PMID:1845973  
A:Accession: A39043  
A:Molecule type: protein  
A:Residues: 26-51, 1-53 <STA>  
A:Experimental source: cultured embryonic fibroblasts infected with Rous sarcoma virus  
A:Note: contains disulfide bonds; not glycosylated; has inhibitory activity  
C:Function:  
A:Description: regulation of extracellular matrix remodeling by inhibition of matrix metalloproteinase  
A:Note: transcription induced by cytokines, tumor promoters, and anti-inflammatory agents  
A:Note: TIMP-1 and TIMP-3 have distinct but overlapping tissue-specific expression patterns  
C:Superfamily: metalloproteinase inhibitor  
C:Keywords: extracellular matrix; glycoprotein; metalloproteinase inhibitor  
F:1-24/Domain: signal sequence #status predicted <SIG>  
F:25-212/Product: metalloproteinase inhibitor 3 #status experimental <MAT>  
F:25-92,27-119,37-144,146-193,151-156,164-185/Disulfide bonds: #status predicted  
F:208/Binding site: carboxylate (Asn) (covalent) #status absent

Query Match 37.8%; Score 381.5; DB 1; Length 212;  
Best Local Similarity 40.1%; Pred. No. 7.2e-31; Mismatches 67; Indels 7; Gaps 4;  
Matches 71; Conservative 32; Mismatches 67; Indels 7; Gaps 4;

Qy 1 CTCVPPHPQTAFCSNLDIVIRAKFVGTPEVNO-TTL-YQRYEIKMTVMKYGFGQALGDAADIR 59  
Db 25 CTCVPIHQDAFCNSDIVIRAKVCKLMDKDPFGTMRVTVMKMGVGFQIM---PHVQ 81  
Qy 60 FVYTPAMESVCGYFHRSHNRSEFLIAGLQDLHLHTTCFSFVAPWNSLSLAQRGFTKT 119  
Db 82 YIYTEASESLCGV---KLVNKYQYLITGRVYEGKVYGLNWKYKWDRLTSLQKGLNHR 139  
Qy 120 YTVGCECTVFPCLSTPCKLQSGTHCLWTDLLQSGKGFQSRHLACLPRPGLCTW 176  
Db 140 YHLGC-GCKIRPCYILPCFATSKNECIWMLSNFGSHGQAKHYACIQRVGYCSW 195

RESULT 12  
S38624  
Metalloproteinase inhibitor 2 precursor - long-tailed hamster (fragment)  
N:Alternate names: TIMP-2; tissue inhibitor of metalloproteinases 2  
C:Species: Cricetulus longicaudatus (long-tailed hamster)  
C:Date: 06-Jan-1995 #sequence\_revision 12-Apr-1996 #text\_change 18-Jun-1999  
A:Accession: S38624  
R:Suzuki, Y.  
Submitted to the EMBL Data Library, November 1993  
A:Reference number: S38624  
A:Accession: S38624  
A:Molecule type: mRNA  
A:Residues: 1-196 <SUZ>  
A:Cross-references: EMBL:X75924; NID:G414876; PIDN:CAA53528.1; PID:G414877  
C:Function:  
A:Description: regulation of extracellular matrix remodeling by inhibition of matrix metalloproteinase  
possibly controlling their activation; TIMP-1 and TIMP-2 possess erythroid potentiating  
C:Superfamily: metalloproteinase inhibitor  
C:Keywords: erythropoiesis; extracellular matrix; metalloproteinase inhibitor; mitogen  
F:3-196/Product: metalloproteinase inhibitor 2 #status predicted <MAT>  
F:3-74,5-103,15-128,130-177,135-140,148-169/Disulfide bonds: #status predicted

Query Match 37.6%; Score 379.5; DB 1; Length 196;  
Best Local Similarity 41.8%; Pred. No. 1e-30;  
Matches 77; Conservative 26; Mismatches 66; Indels 15; Gaps 6;

Qy 1 CTCVPPHPQTAFCSNLDIVIRAKFVGTPEVNO-TTLQY-----RYEIKMTVMKYGFGQALG 53  
Db 3 CSCSPVHPQQAFCNADVIRAKVSEKVDGNDIYGNPIKRIQVEIKRMFK-----G 57  
Qy 54 DAADIRFVYTPAMESVCGYFHRSHNRSEFLIAGLQ-DGLLHITTCFSFVAPWNSLSLAQ 112  
Db 58 PKDIEFITYAPSSAVCG-VSLDVGGKKKEYLIAGKAEQDKWHITLCDFIWPDLTSTTQ 116

Qy 113 RRGFTKTYTVGCECTVFPCLSTPCKLQSGTHCLWTDLLQSGKGFQSRHLACLPRPBG 172  
Db 117 KKSLSNHRVQMGCG-ECKITRCMPICYISSPDECLWMDWVTEKSIHQAKFFACIKRSDG 175  
Qy 173 LCTW 176  
Db 176 SCAM 179

RESULT 13  
S45683  
Metalloproteinase inhibitor 2 precursor - rat  
N:Alternate names: TIMP-2; tissue inhibitor of metalloproteinases 2  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
A:Accession: S45683; S20325; S60160  
R:Cook, T.P.; Burke, J.S.; Bergman, K.D.; Quinn, C.O.; Jeffrey, J.J.; Partridge, N.C.  
Arch. Biochem. Biophys. 311, 313-320, 1994  
A:Title: Cloning and regulation of rat tissue inhibitor of metalloproteinases-2  
A:Reference number: S45683; MUID:94263207; PMID:8203893  
A:Accession: S45683  
A:Molecule type: mRNA  
A:Residues: 1-220 <COO>  
A:Cross-references: GB:U14526; NID:G540204; PIDN:AAA21553.1; PID:G540205  
R:Roswit, W.T.; McCourt, D.W.; Partridge, N.C.; Jeffrey, J.J.  
Arch. Biochem. Biophys. 292, 402-410, 1992  
A:Title: Purification and sequence analysis of two rat tissue inhibitors of metalloproteinases-2  
A:Reference number: S20325; MUID:92117648; PMID:1309971  
A:Accession: S20325  
A:Molecule type: protein  
A:Residues: 27-48 <ROS>  
R:Gibbons, K.L.; O'Grady, R.L.; Piper, A.A.  
Submitted to the EMBL Data Library, June 1995  
A:Description: Rat tissue inhibitor of metalloproteinases-2: cDNA cloning and sequence  
A:Reference number: S60160  
A:Accession: S60160  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-6, 'S', 8-20, 'V', 22-152, 'E', 154-220 <GIB>  
A:Cross-references: EMBL:L31884  
C:Genetics:  
A:Gene: TIMP-2  
C:Function:  
A:Description: regulation of extracellular matrix remodeling by inhibition of matrix metalloproteinase  
possibly controlling their activation; TIMP-1 and TIMP-2 possess erythroid potentiating  
C:Superfamily: metalloproteinase inhibitor  
C:Keywords: erythropoiesis; extracellular matrix; metalloproteinase inhibitor; mitogen  
F:1-26/Domain: signal sequence #status predicted <SIG>  
F:1-220/Product: metalloproteinase inhibitor 2 #status predicted <MAT>  
F:27-98,129-127,39-152,154-201,159-164,172-193/Disulfide bonds: #status predicted

Query Match 37.6%; Score 379.5; DB 1; Length 220;  
Best Local Similarity 41.3%; Pred. No. 1.2e-30;  
Matches 76; Conservative 28; Mismatches 65; Indels 15; Gaps 6;

Qy 1 CTCVPPHPQTAFCSNLDIVIRAKFVGTPEVNO-TTLQY-----RYEIKMTVMKYGFGQALG 53  
Db 27 CSCSPVHPQQAFCNADVIRAKVSEKVDGNDIYGNPIKRIQVEIKRMFK-----G 81  
Qy 54 DAADIRFVYTPAMESVCGYFHRSHNRSEFLIAGLQ-DGLLHITTCFSFVAPWNSLSLAQ 112  
Db 82 PKDIEFITYAPSSAVCG-VSLDVGGKKKEYLIAGKAEQDKWHITLCDFIWPDLTSTTQ 140  
Qy 113 RRGFTKTYTVGCECTVFPCLSTPCKLQSGTHCLWTDLLQSGKGFQSRHLACLPRPBG 172  
Db 141 KKSLSNHRVQMGCG-ECKITRCMPICYISSPDECLWMDWVTEKSIHQAKFFACIKRSDG 199  
Qy 173 LCTW 176  
Db 200 SCAM 203

RESULT 14



545317  
metalloproteinase inhibitor 3 precursor [validated] - human  
N:Alternate names: mlg-5 protein; TIMP-3; tissue inhibitor of metalloproteinases 3  
C:Species: Homo sapiens (man)  
C:Date: 06-Jan-1995 #sequence revision 12-Apr-1996 #text change 08-Dec-2000  
A:Accession: S45317; S59515; S53870; I38023; A49614; C56937; I53025; S47041  
R:Urita, J.A.; Ferrando, A.A.; Velasco, G.; Freije, J.M.P.; Lopez-Otin, C.  
Cancer Res. 54, 2091-2094, 1994  
A:Title: Structure and expression in breast tumors of human TIMP-3, a new member of the  
A:Reference number: S45317; MUID:94228524; PMID:8174111  
A:Accession: S45317  
A:Molecule type: mRNA  
A:Residues: 1-211 <URI>  
A:Cross-references: EMBL:X76227; NID:S495251; PIDD:CAA53813.1; PID:S495252  
A:Experimental source: breast tumor cDNA library  
R:Silbiger, S.M.; Jacobsen, V.L.; Cupples, R.L.; Koski, R.A.  
Gene 141, 293-297, 1994  
A:Title: Cloning of cDNAs encoding human TIMP-3, a novel member of the tissue inhibitor  
A:Reference number: S59515; MUID:94215920; PMID:8163205  
A:Accession: S59515  
A:Molecule type: protein  
A:Residues: 1-211 <URI>  
A:Cross-references: EMBL:U02571; NID:S472309; PIDD:AA17672.1; PID:S472310  
R:Kishanani, N.S.; Staskus, P.W.; Yang, T.T.; Mastarz, F.R.; Hawkes, S.P.  
Matrix Biol. 11, 479-488, 1994  
A:Title: Identification and characterization of human tissue inhibitor of metalloprotein  
A:Reference number: S53870  
A:Accession: S53870  
A:Molecule type: protein  
A:Residues: 'X',25,'XX',28,'X',30-35,'X',37,'X',39-41 <KIS>  
R:Wick, M.; Burger, C.; Brueselbach, S.; Lucibello, F.C.; Mueller, R.  
J. Biol. Chem. 269, 18953-18960, 1994  
A:Title: A novel member of human tissue inhibitor of metalloproteinases (TIMP) gene family  
A:Reference number: I38023; MUID:94308155; PMID:8034652  
A:Accession: I38023  
A:Molecule type: mRNA  
A:Residues: 1-15,'W',17,'T',20-21,'PR',24-201,'X',203-211 <RES>  
A:Cross-references: EMBL:J20183; NID:S520931; PIDD:CAA82918.1; PID:S520932  
A:Experimental source: fibroblast cell line WI-38  
R:Apte, S.S.; Matei, M.G.; Olsen, B.R.  
Genomics 19, 86-90, 1994  
A:Title: Cloning of the cDNA encoding human tissue inhibitor of metalloproteinases-3 (TIMP  
A:Reference number: A49614; MUID:94245184; PMID:8188246  
A:Accession: A49614  
A:Molecule type: mRNA  
A:Residues: 14-20,'R',23-211 <APT>  
A:Cross-references: GB:U15078; NID:g407034; PIDD:AAA21815.1; PID:g407035  
A:Experimental source: placenta cDNA library  
R:Apte, S.S.; Olsen, B.R.; Murphy, G.  
J. Biol. Chem. 270, 14313-14318, 1995  
A:Title: The gene structure of tissue inhibitor of metalloproteinases (TIMP)-3 and its i  
A:Reference number: A56937; MUID:95301511; PMID:7782289  
A:Accession: C56937  
A:Molecule type: protein  
A:Residues: 'X',25,'X',27-35,'X',37 <AP2>  
R:Wilde, C.G.; Hawkins, P.R.; Coleman, R.T.; Levine, W.B.; Deleage, A.M.; Okamoto, P.M.  
DNA Cell Biol. 13, 711-718, 1994  
A:Title: Cloning and characterization of human tissue inhibitor of metalloproteinases-3  
A:Reference number: I53025; MUID:95290091; PMID:7772252  
A:Accession: I53025  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-211 <R2>  
A:Cross-references: GB:S78453; NID:g998825; PIDD:AA34532.1; PID:g998826  
C:Genetics:  
A:Gene: GDB:TIMP3  
A:Cross-references: GDB:138175; OMIM:188826  
A:Map position: 22q12.1-22q13.2  
C:Function:  
A:Description: regulation of extracellular matrix remodeling by inhibition of matrix met  
A:Note: TIMP-1 and TIMP-3 have distinct but overlapping tissue-specific expression pattern

C:Superfamily: metalloproteinase inhibitor  
C:Keywords: extracellular matrix; metalloproteinase inhibitor  
F:1-23/Domains: signal sequence #status predicted <SIS>  
F:24-211/Product: metalloproteinase inhibitor 3 #status experimental <MAT>  
F:24-91,26-118,36-143,145-192,150-155,163-184/disulfide bonds: #status predicted

	Query Match	37.4%	Score 377.5;	DB 1;	Length 211;
	Best Local Similarity	40.8%;	Pred. No. 1,8e+30;		
	Matches 73;	Conservative 33;	Mismatches 62;	Indels 11;	Gaps 5;

Oy 1 CTCVPHPTACNSNDLVRAKFFVTPEVNO--TTLQRYEIKMTMYGFGALDAAD 57  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 24 CTCSSHDPDACCNSDIVIRAKVGVKKLVEGFGLLV--YTIKOMGMVGFTGM---PH 78  
::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::  
Oy 58 IREVVTPAMESVCGYFHRSNHSSEFLNGKLODLHLHTTCSPFAWMSLSLAQRGFT 117  
::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::  
Db 79 VQYIHTAESIESICGL--KLEVNKYQYLLTGVRVDGKMGTGLCNFVERMDQLTTSQRKGLN 136  
::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::  
Oy 118 KIVTVGCBCETVFPCILSIKCTKLGSTGHCLMTPDLLGSSEKGFPSRHLACLPREGLCITW 176  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 137 YRHLYGC-NCKTKSCYLCEPVTISKNECLMTDMLSNPGYPGVSGKHAYCIHQKGVCISW 194  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 15  
A37128  
metalloproteinase inhibitor 2 precursor [validated] - human  
N:Alternate names: chondrocyte-derived angiogenesis inhibitor; TIMP-2; tissue inhibitor C  
C:Species: Homo sapiens (man)  
C>Date: 08-Mar-1991 #sequence revision 12-Apr-1996 #ext change 08-Dec-2000  
C:Date: 08-Mar-1991 #sequence revision 12-Apr-1996 #ext change 08-Dec-2000  
C:Accession: A37128; B35996; A34464; A34415; S21303; S20319; S17165; S58794  
C:Stetler-Stevenson, W.G.; Brown, P.D.; Onisto, M.; Levy, A.T.; Liotta, L.A.  
J. Biol. Chem. 265, 13933-13938, 1990  
A>Title: Tissue inhibitor of metalloproteinases-2 (TIMP-2) mRNA expression in tumor cell  
A:Reference number: A37128; PMID:90338014; PMID:2380196  
A:Accession: A37128  
A:Molecule type: mRNA  
A:Residues: 1-220 <STE>  
A:Cross-references: GB:J05593; NID:g339706; PID:NAAA61186.1; PID:g339707  
A:Experimental source: A2058 melanoma cell CDNA library  
J:Boone, T.C.; Johnson, M.J.; De Clerck, Y.A.; Langley, K.E.  
Proc. Natl. Acad. Sci. U.S.A. 87, 2800-2804, 1990  
A>Title: cDNA cloning and expression of a metalloproteinase inhibitor related to tissue i  
A:Reference number: A35996; PMID:90207285; PMID:2157214  
A:Accession: B35996  
A:Molecule type: mRNA  
A:Residues: 1-220 <BOO>  
A:Cross-references: GB:M2304; NID:g187522; PID:NAAA9581.1; PID:g307195  
A:Experimental source: fetal aorta cDNA library  
J:Stetler-Stevenson, W.G.; Kruttsch, H.C.; Liotta, L.A.  
J. Biol. Chem. 264, 1374-1378, 1989  
A>Title: Tissue inhibitor of metalloproteinase (TIMP-2). A new member of the metalloprote  
A:Reference number: A34464; PMID:9008902; PMID:2793861  
A:Accession: A34464  
A:Molecule type: protein  
A:Residues: 27-77,'K','79-81','I','83-100','E','102-117','119-121','R','123-149','Q','151-174','T','1'  
A:Experimental source: serum-free culture medium of A2058 cells  
J:Goldberg, G.I.; Marner, B.L.; Grant, G.A.; Eisen, A.Z.; Wilhelm, S.; He, C.  
Proc. Natl. Acad. Sci. U.S.A. 86, 8207-8211, 1989  
A>Title: Human 72-kilodalton type IV collagenase forms a complex with a tissue inhibitor  
A:Reference number: A34415; PMID:90046765; PMID:2554304  
A:Accession: A34415  
A:Molecule type: protein  
A:Residues: 30-51;124-141;159-173 <COL>  
A:Submitted to the EMBL Data Library, August 1990  
A:Description: Nucleotide sequence of a TIMP-II cDNA.  
A:Reference number: S21303  
A:Accession: S21303  
A:Molecule type: mRNA  
A:Residues: 30-95,'V','97-214 <MAL>  
A:Cross-references: EMBL:X54533; NID:g37180; PID:CA38400.1; PID:g37181  
J:Oschneck, A.; Krauter, V.; Oberhoff, R.; Reinke, H.; Tschesche, H.  
FEBS Lett. 296, 16-20, 1992

A:Title: Isolation and characterization of tissue inhibitors of metalloproteinases (TIMP)  
A:Reference number: S20318; MUID:92111776; PMID:1730286  
A:Accession: S20319  
A:Molecule type: protein  
A:Residues: 'X',28,'X',30-38,'X',40-41 <OST>  
A:Experimental source: rheumatoid synovial fluid  
R:Ward, R.V.; Hembray, R.M.; Reynolds, J.J.; Murphy, G.  
Biochem. J. 278, 179-187, 1991  
A:Title: The purification of tissue inhibitor of metalloproteinases-2 from its 72 kDa protein  
A:Reference number: S17165; MUID:91354200; PMID:1909113  
A:Accession: S17165  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 27,'X',29,'X',31-38 <WAR>  
R:Ohba, Y.; Goto, Y.; Kimura, Y.; Suzuki, F.; Hisa, T.; Takahashi, K.; Takigawa, M.  
Biochim. Biophys. Acta 1245, 1-8, 1995  
A:Title: Purification of an angiogenesis inhibitor from culture medium conditioned by a  
A:Reference number: S58794; MUID:95383380; PMID:7544625  
A:Accession: S58794  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 27-37 <OHB>  
C:Genetics:  
A:Gene: GDB:TIMP2  
A:Cross-references: GDB:132612; OMIM:188825  
A:Map position: 17q25-17q25  
C:Function:  
A:Description: regulation of extracellular matrix remodeling by inhibition of matrix metalloproteinases  
possibly controlling their activation; TIMP-1 and TIMP-2 possess erythroid potentiating  
C:Superfamily: metalloproteinase inhibitor  
C:Keywords: erythropoiesis; extracellular matrix; metalloproteinase inhibitor; mitogen  
F:1-26/Domain: signal sequence #status predicted <SIG>  
F:27-220/Product: metalloproteinase inhibitor 2 #status experimental <MAT>  
F:27-98,29-127,39-152,154-201,159-164,172-193/Disulfide bonds: #status predicted

Query Match 37.4%; Score 377.5; DB 1; Length 220;  
Best Local Similarity 41.3%; Pred. No. 1.9e-30;  
Matches 76; Conservative 27; Mismatches 66; Indels 15; Gaps 6;

QY	1	CTCVPHPQTAFCNSDLVIRAFVGTPEVNO-TTLYQ-----RYEIKMTKMYKGFQALG	53
DB	27	CSCSPVHPQQAFCNADVIRAKAVSEKVDSCNDIVGNPIKEIQYIKIMFK-----G	81
QY	54	DAADIRFVYTPAMESVCGYFHRSHNRSEFLIAGKLQ-DGLLHITTCSPVAPWNSLSLAQ	112
DB	82	PEKDIEFIYTPASSAVCG-VSLDVGKKKEYLIAGKAEKDGKMHITLCDPFIVPWDTLSTTQ	140
QY	113	RRGFTKTYTVGCECTVPCLSPCKLQSGTHCLWTDLQSGSEKGFQSRHLACLPREPG	172
DB	141	KKSLNHYQMGCECKITRCPMIPCVISSPDECLWMDWVTEKNINGHOAKFFACIKRSDG	199
QY	173	LCTW	176
DB	200	SCAW	203

Search completed: December 17, 2002, 15:07:09  
Job time : 19.4 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: December 17, 2002, 15:04:26 ; Search time 10.1517 Seconds  
(without alignments)  
751.758 Million cell updates/sec

Title: US-09-452-817-1

Perfect score: 1009  
Sequence: 1 CTCVPHPHQTAFCNSDLVIR.....ACLPREGLCTWOSLRQIA 184

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1009	100.0	207	1	TIM1_HUMAN
2	1002	99.3	207	1	TM1_PAPCY
3	989	98.0	207	1	TM1_MACMU
4	893	88.5	207	1	TM1_BOVIN
5	876	86.8	207	1	TM1_SHEEP
6	866	85.8	207	1	TM1_RIG
7	826	81.9	207	1	TM1_HORSE
8	817.5	81.0	206	1	TM1_RABIT
9	811	80.4	207	1	TM1_CANFA
10	761.5	75.5	205	1	TM1_MOUSE
11	742	73.5	217	1	TM1_RAT
12	388.5	38.5	214	1	TM3_SCYTO
13	383.5	38.0	220	1	TM2_CHICK
14	382.5	37.9	220	1	TM2_MOUSE
15	382.5	37.9	220	1	TM2_RAT
16	381.5	37.8	212	1	TM3_CHICK
17	380.5	37.7	220	1	TM2_CAVPO
18	379.5	37.6	196	1	TM2_CAVPO
19	379.5	37.6	214	1	TM3_CRILLO
20	378.5	37.5	211	1	TM3_XENLA
21	377.5	37.4	211	1	TM3_HORSE
22	377.5	37.4	220	1	TM3_HUMAN
23	374.5	37.1	220	1	TM2_CANFA
24	373.5	37.0	211	1	TM3_MOUSE
25	372.5	36.9	211	1	TM3_RAT
26	370.5	36.7	220	1	TM2_BOVIN
27	368.5	36.5	211	1	TM2_BOVIN
28	363.5	36.0	194	1	TM2_RABIT
29	360	35.7	224	1	TM4_MOUSE
30	351	34.8	224	1	TM4_HUMAN
31	350	34.7	224	1	TM4_RAT
32	293.5	29.1	151	1	TM3_RABIT
33	291	28.8	170	1	TM4_RABIT

34	208	20.6	107	1	TM4_BOVIN	O97563 bos taurus
35	158	15.7	210	1	TM2_DROME	O97514 drosophila
36	146.5	14.5	91	1	TM2_HORSE	O77717 equus caball
37	88.5	8.8	512	1	HVAL_MOUSE	P48794 mus musculu
38	78	7.7	535	1	PAH2_HUMAN	O15460 homo sapien
39	77.5	7.7	944	1	DNL4_YEAST	O08387 saccharomyc
40	76.5	7.6	183	1	DERM_BOVIN	P19427 bos taurus
41	75.5	7.5	423	1	YGCN_ECOLI	O46904 escherichia
42	75	7.4	461	1	TRIA_RAT	P22934 rattus norv
43	74.5	7.4	430	1	SVH_PORPU	P51348 porphyra pu
44	74.5	7.4	444	1	SKD1_MOUSE	P46467 mus musculu
45	73.5	7.3	444	1	SKD1_HUMAN	O75351 homo sapien

## ALIGNMENTS

RESULT 1	ID	Sequence	Standard	PRT	207 AA.
1	1	1009	100.0	207	1
2	2	1002	99.3	207	1
3	3	989	98.0	207	1
4	4	893	88.5	207	1
5	5	876	86.8	207	1
6	6	866	85.8	207	1
7	7	826	81.9	207	1
8	8	817.5	81.0	206	1
9	9	811	80.4	207	1
10	10	761.5	75.5	205	1
11	11	742	73.5	217	1
12	12	388.5	38.5	214	1
13	13	383.5	38.0	220	1
14	14	382.5	37.9	220	1
15	15	382.5	37.9	220	1
16	16	381.5	37.8	212	1
17	17	380.5	37.7	220	1
18	18	379.5	37.6	196	1
19	19	379.5	37.6	214	1
20	20	378.5	37.5	211	1
21	21	377.5	37.4	211	1
22	22	377.5	37.4	220	1
23	23	374.5	37.1	220	1
24	24	373.5	37.0	211	1
25	25	372.5	36.9	211	1
26	26	370.5	36.7	220	1
27	27	368.5	36.5	211	1
28	28	363.5	36.0	194	1
29	29	360	35.7	224	1
30	30	351	34.8	224	1
31	31	350	34.7	224	1
32	32	293.5	29.1	151	1
33	33	291	28.8	170	1

34	34	208	20.6	107	1	TM4_BOVIN	O97563 bos taurus
35	35	158	15.7	210	1	TM2_DROME	O97514 drosophila
36	36	146.5	14.5	91	1	TM2_HORSE	O77717 equus caball
37	37	88.5	8.8	512	1	HVAL_MOUSE	P48794 mus musculu
38	38	78	7.7	535	1	PAH2_HUMAN	O15460 homo sapien
39	39	77.5	7.7	944	1	DNL4_YEAST	O08387 saccharomyc
40	40	76.5	7.6	183	1	DERM_BOVIN	P19427 bos taurus
41	41	75.5	7.5	423	1	YGCN_ECOLI	O46904 escherichia
42	42	75	7.4	461	1	TRIA_RAT	P22934 rattus norv
43	43	74.5	7.4	430	1	SVH_PORPU	P51348 porphyra pu
44	44	74.5	7.4	444	1	SKD1_MOUSE	P46467 mus musculu
45	45	73.5	7.3	444	1	SKD1_HUMAN	O75351 homo sapien

1	1	1009	100.0	207	1	TM1_HUMAN	P01033 homo sapien
2	2	1002	99.3	207	1	TM1_PAPCY	P49061 papio cynoc
3	3	989	98.0	207	1	TM1_MACMU	O95K19 macaca mula
4	4	893	88.5	207	1	TM1_BOVIN	P20414 bos taurus
5	5	876	86.8	207	1	TM1_SHEEP	P50122 ovis aries
6	6	866	85.8	207	1	TM1_RIG	P35624 sus scrofa
7	7	826	81.9	207	1	TM1_HORSE	O02722 equus caball
8	8	817.5	81.0	206	1	TM1_RABIT	P20614 oryctolagus
9	9	811	80.4	207	1	TM1_CANFA	P81546 canis famil
10	10	761.5	75.5	205	1	TM1_MOUSE	P12032 mus musculu
11	11	742	73.5	217	1	TM1_RAT	P30120 rattus norv
12	12	388.5	38.5	214	1	TM3_SCYTO	O96b4 scyllorhinu
13	13	383.5	38.0	220	1	TM2_CHICK	O42146 gallus gall
14	14	382.5	37.9	220	1	TM2_MOUSE	P25785 mus musculu
15	15	382.5	37.9	220	1	TM2_RAT	P30121 rattus norv
16	16	381.5	37.8	212	1	TM3_CHICK	P26552 gallus gall
17	17	380.5	37.7	220	1	TM2_CAVPO	O9wuc6 cavia porce
18	18	379.5	37.6	196	1	TM2_CAVPO	O60453 cricetus
19	19	379.5	37.6	214	1	TM3_CRILLO	O73746 xenopus lae
20	20	378.5	37.5	211	1	TM3_HORSE	O9u19 equus caball
21	21	377.5	37.4	211	1	TM3_HUMAN	P35625 homo sapien
22	22	377.5	37.4	220	1	TM2_HUMAN	P16035 homo sapien
23	23	374.5	37.1	220	1	TM2_CANFA	O9ctyl1 canis famil
24	24	373.5	37.0	211	1	TM3_MOUSE	P3876 mus musculu
25	25	372.5	36.9	211	1	TM3_RAT	P48032 rattus norv
26	26	370.5	36.7	220	1	TM2_BOVIN	P16368 bos taurus
27	27	368.5	36.5	211	1	TM2_BOVIN	P79121 bos taurus
28	28	363.5	36.0	194	1	TM2_RABIT	O9rct7 oryctolagus
29	29	360	35.7	224	1	TM4_MOUSE	O9jbt7 mus musculu
30	30	351	34.8	224	1	TM4_HUMAN	O99727 homo sapien
31	31	350	34.7	224	1	TM4_RAT	P81556 rattus norv
32	32	293.5	29.1	151	1	TM3_RABIT	O97590 oryctolagus
33	33	291	28.8	170	1	TM4_RABIT	O97591 oryctolagus

34	34	208	20.6	107	1	TM4_BOVIN	O97563 bos taurus
35	35	158	15.7	210	1	TM2_DROME	O97514 drosophila
36	36	146.5	14.5	91	1	TM2_HORSE	O77717 equus caball
37	37	88.5	8.8	512	1	HVAL_MOUSE	P48794 mus musculu
38	38	78	7.7	535	1	PAH2_HUMAN	O15460 homo sapien
39	39	77.5	7.7	944	1	DNL4_YEAST	O08387 saccharomyc
40	40	76.5	7.6	183	1	DERM_BOVIN	P19427 bos taurus
41	41	75.5	7.5	423	1	YGCN_ECOLI	O46904 escherichia
42	42	75	7.4	461	1	TRIA_RAT	P22934 rattus norv
43	43	74.5	7.4	430	1	SVH_PORPU	P51348 porphyra pu
44	44	74.5	7.4	444	1	SKD1_MOUSE	P46467 mus musculu
45	45	73.5	7.3	444	1	SKD1_HUMAN	O75351 homo sapien

1	1	1009	100.0	207	1	TM1_HUMAN	P01033 homo sapien
2	2	1002	99.3	207	1	TM1_PAPCY	P49061 papio cynoc
3	3	989	98.0	207	1	TM1_MACMU	O95K19 macaca mula
4	4	893	88.5	207	1	TM1_BOVIN	P20414 bos taurus
5	5	876	86.8	207	1	TM1_SHEEP	P50122 ovis aries
6	6	866	85.8	207	1	TM1_RIG	P35624 sus scrofa
7	7	826	81.9	207	1	TM1_HORSE	O02722 equus caball
8	8	817.5	81.0	206	1	TM1_RABIT	P20614 oryctolagus
9	9	811	80.4	207	1	TM1_CANFA	P81546 canis famil
10	10	761.5	75.5	205	1	TM1_MOUSE	P12032 mus musculu
11	11	742	73.5	217	1	TM1_RAT	P30120 rattus norv
12	12	388.5	38.5	214	1	TM3_SCYTO	O96b4 scyllorhinu
13	13	383.5	38.0	220	1	TM2_CHICK	O42146 gallus gall
14	14	382.5	37.9	220	1	TM2_MOUSE	P25785 mus musculu
15	15	382.5	37.9	220	1	TM2_RAT	P30121 rattus norv
16	16	381.5	37.8	212	1	TM3_CHICK	P26552 gallus gall
17	17	380.5	37.7	220	1	TM2_CAVPO	O9wuc6 cavia porce
18	18	379.5	37.6	196	1	TM2_CAVPO	O60453 cricetus
19	19	379.5	37.6	214	1	TM3_CRILLO	O73746 xenopus lae
20	20	378.5	37.5	211	1	TM3_HORSE	O9u19 equus caball
21	21	377.5	37.4	211	1	TM3_HUMAN	P35625 homo sapien
22	22	377.5	37.4	220	1	TM2_HUMAN	P16035 homo sapien
23	23	374.5	37.1	220	1	TM2_CANFA	O9ctyl1 canis famil
24	24	373.5	37.0	211	1	TM3_MOUSE	P3876 mus musculu
25	25	372.5	36.9	211	1	TM3_RAT	P48032 rattus norv
26	26	370.5	36.7	220	1	TM2_BOVIN	P16368 bos taurus
27	27	368.5	36.5	211	1	TM2_BOVIN	P79121 bos taurus
28	28	363.5	36.0	194	1	TM2_RABIT	O9rct7 oryctolagus
29	29	360	35.7	224	1	TM4_MOUSE	O9jbt7 mus musculu
30	30	351	34.8	224	1	TM4_HUMAN	O99727 homo sapien
31	31	350	34.7	224	1	TM4_RAT	P81556 rattus norv
32	32	293.5	29.1	151	1	TM3_RABIT	O97590 oryctolagus
33	33	291	28.8	170	1	TM4_RABIT	O97591 oryctolagus

34	34	208	20.6	107	1	TM4_BOVIN	O97563 bos taurus
35	35	158	15.7	210	1	TM2_DROME	O97514 drosophila



OY 181 SOIA 184  
Db 204 SOIA 207

## RESULT 2

TM1\_PAPCY STANDARD; PRT: 207 AA.  
ID ID TM1\_PAPCY STANDARD; PRT: 207 AA.  
AC P49061;  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Metalloproteinase inhibitor 1 precursor (TIMP-1).  
GN TIMP1.  
OS Papio cynocephalus (Yellow baboon).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Papio.  
NCBI\_TaxID=9556;  
RP SEQUENCE FROM N.A.  
RC TISSUE=Arteria;  
RX MEDLINE=96011646; PubMed=7590279;  
RA Forough R., Nikkari S.T., Hasenstab D., Lea H., Clowes A.W.;  
RT "Cloning and characterization of a cDNA encoding the baboon tissue inhibitor of matrix metalloproteinase-1 (TIMP-1)."  
RL Gene 163:267-271(1995).  
CC -1- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES) AND IRREVERSIBLY INACTIVATES THEM.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- PTM: THE ACTIVITY OF TIMP-1 IS DEPENDENT ON THE PRESENCE OF DISULFIDE BONDS.  
CC -1- SIMILARITY: BELONGS TO THE TIMP FAMILY.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; L37295; AAA99943.1; -  
CC HSSP; P01033; ID2B.  
CC InterPro: IPR001820; TIMP.  
CC Pfam; PF00965; TIMP; 1.  
CC SMART; SM00206; TIMP; 1.  
CC PROSITE; PS00288; TIMP; 1.  
CC Glycoprotein; Metalloproteinase inhibitor; Erythrocyte maturation; Signal.  
CC Signal.  
CC CHAIN 1 23 BY SIMILARITY.  
CC DISULFID 24 207 METALLOPROTEINASE INHIBITOR 1.  
CC DISULFID 24 93 BY SIMILARITY.  
CC DISULFID 26 122 BY SIMILARITY.  
CC DISULFID 36 147 BY SIMILARITY.  
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CC DISULFID 155 160 BY SIMILARITY.  
CC DISULFID 168 189 BY SIMILARITY.  
CC CARBOHYD 53 53 N-LINKED (GLCNAC... ) (POTENTIAL).  
CC CARBOHYD 101 101 N-LINKED (GLCNAC... ) (POTENTIAL).  
CC SEQUENCE 207 AA; 23213 MW; 5AB4FDBEAB2ECDC CRC64;

Query Match 99.3%; Score 1002; DB 1; Length 207;  
Best Local Similarity 98.9%; Pred. No. 1.1e-96;  
Matches 182; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTCVPHPHOTAFCSNDIVIRAKFVGTPEVNOTTLVORVEIKTKTKYKGFQALGDAADIRF 60  
Db 24 CTCVPHPHOTAFCSNDIVIRAKFVGTPEVNOTTLVORVEIKTKTKYKGFQALGDAADIRF 83  
OY 61 VTPAMESVCGYFHRSHNSEEFLLAGKLQDGLLHITTCSPVAPWNSLSLAORRGFTKTY 120  
Db 84 VTPAMESVCGYFHRSHNSEEFLLAGKLQDGLLHITTCSPVAPWNSLSLAORRGFTKTY 143

OY 121 TWGCECTVFPCLSIIPCKLQSGTHCLMTDOLQSGSEKGFOSRHLACLPRPGLCTWOSLR 180  
Db 144 TWGCECTVFPCLSIIPCKLQSGTHCLMTDOLQSGSEKGFOSRHLACLPRPGLCTWOSLR 203

OY 181 SOIA 184  
Db 204 TRIA 207

## RESULT 3

TM1\_MACMU STANDARD; PRT: 207 AA.  
ID ID TM1\_MACMU STANDARD; PRT: 207 AA.  
AC Q95KLE9;  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DE Metalloproteinase inhibitor 1 precursor (TIMP-1).  
GN TIMP1.  
OS Macaca mulatta (Rhesus macaque).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Macaca.  
NCBI\_TaxID=9544;  
RP SEQUENCE FROM N.A.  
RC TISSUE=Placenta;  
RX Ji S., Wang Y., Li H., Ji W., Piao Y.;  
RT "Cloning and characterization of tissue inhibitor of matrix metalloproteinase-1 (TIMP-1) cDNA from Macaca mulatta."  
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES) AND IRREVERSIBLY INACTIVATES THEM.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- PTM: THE ACTIVITY OF TIMP-1 IS DEPENDENT ON THE PRESENCE OF DISULFIDE BONDS.  
CC -1- SIMILARITY: BELONGS TO THE TIMP FAMILY.  
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CC -----  
CC EMBL; AF366397; AAK53704.1; -  
CC InterPro: IPR001820; TIMP.  
CC Pfam; PF00965; TIMP; 1.  
CC PROSITE; PS00288; TIMP; FALSE NEG.  
CC Glycoprotein; Metalloproteinase inhibitor; Erythrocyte maturation; Signal.  
CC Signal.  
CC CHAIN 1 23 BY SIMILARITY.  
CC DISULFID 24 207 METALLOPROTEINASE INHIBITOR 1.  
CC DISULFID 24 93 BY SIMILARITY.  
CC DISULFID 26 122 BY SIMILARITY.  
CC DISULFID 36 147 BY SIMILARITY.  
CC DISULFID 150 197 BY SIMILARITY.  
CC DISULFID 155 160 BY SIMILARITY.  
CC DISULFID 168 189 BY SIMILARITY.  
CC CARBOHYD 53 53 N-LINKED (GLCNAC... ) (POTENTIAL).  
CC CARBOHYD 101 101 N-LINKED (GLCNAC... ) (POTENTIAL).  
CC SEQUENCE 207 AA; 23247 MW; 46E227D2AAB580 CRC64;

Query Match 98.0%; Score 989; DB 1; Length 207;  
Best Local Similarity 97.8%; Pred. No. 2.4e-95;  
Matches 180; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 CTCVPHPHOTAFCSNDIVIRAKFVGTPEVNOTTLVORVEIKTKTKYKGFQALGDAADIRF 60  
Db 24 CTCVPHPHOTAFCSNDIVIRAKFVGTPEVNOTTLVORVEIKTKTKYKGFQALGDAADIRF 83  
OY 61 VTPAMESVCGYFHRSHNSEEFLLAGKLQDGLLHITTCSPVAPWNSLSLAORRGFTKTY 120

```

Db 84 VYTPAMESVCGYFHRSHNRSEEFLLAGKLDGLLHITTCFVAPWNSLSLAQRGFTKTY 143
Qy 121 TVGCECTVFPCLSPCKLQSGTHCLWTDQLQSGSEKGFQSRHLACLPRPGLCTWQSLR 180
Db 144 TVGCECTVFPCLSPCKLQSGTHCLWTDQLQSGSEKGFQSRHLACLPRPGLCTWQSLR 203
Qy 181 SQIA 184
Db 204 TRMA 207

RESULT 4
TIM1_BOVIN STANDARD; PRT; 207 AA.
AC P20414; Q3TVB0;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Metalloproteinase inhibitor 1 precursor (TIMP-1) (Embryogenin-1) (EG-1).
GN TIMP1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90365711; PubMed=2393392;
RA Freudenstein J., Wagner S., Luck R.M., Einspanier R., Scheit K.H.;
RT "mRNA of bovine tissue inhibitor of metalloproteinase: sequence and expression in bovine ovarian tissue.";
RL Biochem. Biophys. Res. Commun. 171:250-256(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94257757; PubMed=8199264;
RA Satoh T., Kobayashi K., Yamashita S., Kikuchi M., Sendai Y., Hoshi H.;
RT "Tissue inhibitor of metalloproteinases (TIMP-1) produced by granulosa and oviduct cells enhances in vitro development of bovine embryo.";
RL Biol. Reprod. 50:835-844(1994).
RN [3]
RP SEQUENCE OF 25-191 FROM N.A.
RC TISSUE=Skeletal muscle;
RA Balcerzak D., Querengesser L., Dixon W.T., Baracos V.E.;
RT "Involvement of fibroblasts and muscle cells in the expression of an extracellular proteolytic cascade in bovine skeletal muscle.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP PRELIMINARY SEQUENCE OF 24-69.
RX MEDLINE=90008914; PubMed=2551303;
RA de Clerck Y.A., Yean T.D., Ratzkin B.J., Lu H.S., Langley K.E.;
RT "Purification and characterization of two related but distinct metalloproteinase inhibitors secreted by bovine aortic endothelial cells.";
RL J. Biol. Chem. 264:17445-17453(1989).
CC -!- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES) AND IRREVERSIBLY INACTIVATES THEM.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: THE ACTIVITY OF TIMP-1 IS DEPENDENT ON THE PRESENCE OF DISULFIDE BONDS.
CC -!- SIMILARITY: BELONGS TO THE TIMP FAMILY.
CC
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CC
CC EMBL; M60073; AAA30784.1; -.

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DR EMBL; S70841; AAB30892.1; -.
DR EMBL; AF144763; AAD30303.1; -.
DR PIR; A35685; A35685.
DR PIR; B34468; B34468.
DR HSP; P01033; IUEA.
DR InterPro; IPR001820; TIMP.
DR Pfam; PF00965; TIMP.1.
DR SMART; SM00206; TIMP.1.
DR PROSITE; PS00286; TIMP.1.
KW Glycoprotein; Metalloprotease inhibitor; Erythrocyte maturation;
KW Signal.
FT SIGNAL 1 23 METALLOPROTEINASE INHIBITOR 1.
FT CHAIN 24 207 BY SIMILARITY.
FT DISULFID 24 93 BY SIMILARITY.
FT DISULFID 26 122 BY SIMILARITY.
FT DISULFID 36 147 BY SIMILARITY.
FT DISULFID 150 197 BY SIMILARITY.
FT DISULFID 155 160 BY SIMILARITY.
FT DISULFID 168 189 BY SIMILARITY.
FT CARBOHYD 53 53 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 101 101 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 207 AA; E672BEE2E865F3F7 CRC64;

Query Match 88.5%; Score 893; DB 1; Length 207;
Best Local Similarity 87.0%; Pred. No. 21e-85;
Matches 160; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

Qy 1 CTCVPHPTQATFACNSDLVIRAKFVGTPEVNTQTLTYQRYEIKMTKMYKGFQALGDAADIRF 60
Db 24 CTCVPHPTQATFACNSDVIRAKFVGTAEVNETALYQRYEIKMTKMYKGFQALGDAADIRF 83
Qy 61 VYTPAMESVCGYFHRSHNRSEEFLLAGKLDGLLHITTCFVAPWNSLSLAQRGFTKTY 120
Db 84 IYTPAMESVCGYFHRSHNRSEEFLLAGKLDGLLHITTCFVAPWNSLSLAQRGFTKTY 143
Qy 121 TVGCECTVFPCLSPCKLQSGTHCLWTDQLQSGSEKGFQSRHLACLPRPGLCTWQSLR 180
Db 144 AAGCECTVFPCLSPCKLQSGTHCLWTDQLQSGSEKGFQSRHLACLPRPGLCTWQSLR 203
Qy 181 SQIA 184
Db 204 AQMA 207

RESULT 5
TIM1_SHEEP STANDARD; PRT; 207 AA.
AC P50122;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Metalloproteinase inhibitor 1 precursor (TIMP-1).
GN TIMP1.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Corpus luteum;
RX MEDLINE=94102210; PubMed=8275949;
RA Smith G.W., Goetz T.L., Anthony R.V., Smith M.F.;
RT "Molecular cloning of an ovine ovarian tissue inhibitor of metalloproteinases: ontogeny of messenger ribonucleic acid expression and in situ localization within preovulatory follicles and luteal tissue.";
RL Endocrinology 134:344-352(1994).
CC -!- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES) AND IRREVERSIBLY INACTIVATES THEM.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: THE ACTIVITY OF TIMP-1 IS DEPENDENT ON THE PRESENCE OF DISULFIDE BONDS.
CC

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CC -1- SIMILARITY: BELONGS TO THE TIMP FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL; S67450; AAB29472.1; -  
 CC HSSP; P01033; IUBA.  
 CC InterPro; IPR001820; TIMP.  
 CC Pfam; PF00965; TIMP; 1.  
 CC SMART; SM00206; TIMP; 1.  
 CC PROSITE; PS00288; TIMP; 1.  
 CC Glycoprotein; Metalloprotease inhibitor; Erythrocyte maturation;  
 CC Signal.  
 CC CHAIN 1 23 BY SIMILARITY.  
 CC SIGNAL 1 23 METALLOPROTEINASE INHIBITOR 1.  
 CC FT DISULFID 24 207 BY SIMILARITY.  
 CC FT DISULFID 26 122 BY SIMILARITY.  
 CC FT DISULFID 36 147 BY SIMILARITY.  
 CC FT DISULFID 150 197 BY SIMILARITY.  
 CC FT DISULFID 155 160 BY SIMILARITY.  
 CC FT DISULFID 168 189 BY SIMILARITY.  
 CC FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC SEQUENCE 207 AA; 23057 MW; 1DBCA2012F80E46 CRC64;  
 SO  
 Query Match 86.8%; Score 876; DB 1; Length 207;  
 Best Local Similarity 86.7%; Pred. No. 1,2e-83;  
 Matches 156; Conservative 10; Mismatches 14; Indels 0; Gaps 0;  
 QY 1 CTCVPHPQTAFCSNDLYIRAKFGTPEVNOTTLRYREIKMTKMYKGFQALGDAADIRF 60  
 DB 24 CTCVPHPQTAFCSNDLYIRAKFGTPEVNOTTLRYREIKMTKMYKGFQALGDAADIRF 83  
 QY 61 VYTPMESVCGYFHRSHNRSEEFLLAGKLDGLHITTCSPVAPNNSLSLAQRGFTKTY 120  
 DB 84 IYTPMESVCGYFHRSHNRSEEFLLAGKLDGLHITTCSPVAPNNSLSLAQRGFTKTY 143  
 QY 121 TVGCECTVFPCLSPCKLQSGTHCLMTDQLQSGSEKFGFQSRHLACLPRFGGLCTWQSLR 180  
 DB 144 AAGCECTVFPCLSPCKLQSGTHCLMTDQLQSGSEKFGFQSRHLACLPRFGGLCTWQSLR 203  
 F. T. 6  
 TIMP1 PIG STANDARD; PRT; 207 AA.  
 ID -TIMP1 PIG STANDARD; PRT; 207 AA.  
 AC P35624; O9TT83; O9TTB9;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Metalloprotease inhibitor 1 precursor (TIMP-1).  
 GN TIMP1.  
 OS Sus scrofa (pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Ovary;  
 RX MEDLINE=92201478; PubMed=1312961;  
 RA Tanaka T., Andoh N., Takeya T., Sato E.;  
 RT "Differential screening of ovarian cDNA libraries detected the  
 RT expression of the porcine collagenase inhibitor gene in functional  
 RT corpora lutea."  
 RL Mol. Cell. Endocrinol. 83:65-71(1992).  
 RP SEQUENCE OF 34-195 FROM N.A.  
 RA Wang J.Y., Baer A.E., Kraus V.B., Setton L.A.;  
 RT "Gene expression level of mmp3 and Timp1 in intervertebral disc.";

RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE OF 37-144 FROM N.A.  
 RC TISSUE=Skin;  
 RA Wang J.F., Boykiv R.H., Reno C.R., Hart D.A., Olson M.E.;  
 RT "Cloning and sequencing of porcine TIMP-1."  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)  
 CC AND IRREVERSIBLY INACTIVATES THEM.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- PTM: THE ACTIVITY OF TIMP-1 IS DEPENDENT ON THE PRESENCE OF  
 CC DISULFIDE BONDS.  
 CC -1- SIMILARITY: BELONGS TO THE TIMP FAMILY.  
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 CC -----  
 CC EMBL; S96211; AAB21865.1; -  
 CC EMBL; AF201726; AAF24348.1; -  
 CC EMBL; AF156029; AAF17354.1; -  
 CC HSSP; P01033; IUBA.  
 CC InterPro; IPR001820; TIMP.  
 CC Pfam; PF00965; TIMP; 1.  
 CC SMART; SM00206; TIMP; 1.  
 CC PROSITE; PS00288; TIMP; 1.  
 CC Glycoprotein; Metalloprotease inhibitor; Erythrocyte maturation;  
 CC Signal.  
 CC CHAIN 1 23 BY SIMILARITY.  
 CC SIGNAL 1 23 METALLOPROTEINASE INHIBITOR 1.  
 CC FT DISULFID 24 207 BY SIMILARITY.  
 CC FT DISULFID 26 122 BY SIMILARITY.  
 CC FT DISULFID 36 147 BY SIMILARITY.  
 CC FT DISULFID 150 197 BY SIMILARITY.  
 CC FT DISULFID 155 160 BY SIMILARITY.  
 CC FT DISULFID 168 189 BY SIMILARITY.  
 CC FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CONFLICT 34 34 A -> P (IN REF. 2).  
 CC FT CONFLICT 37 37 S -> N (IN REF. 3).  
 CC FT CONFLICT 41 41 V -> F (IN REF. 2).  
 CC FT CONFLICT 49 49 K -> Q (IN REF. 1).  
 CC FT CONFLICT 59 59 T -> A (IN REF. 3).  
 CC FT CONFLICT 86 86 EI -> KT (IN REF. 3).  
 CC SEQUENCE 207 AA; 23098 MW; B04895846EB56BD0 CRC64;  
 SO  
 Query Match 85.8%; Score 866; DB 1; Length 207;  
 Best Local Similarity 83.2%; Pred. No. 1,3e-82;  
 Matches 153; Conservative 14; Mismatches 17; Indels 0; Gaps 0;  
 QY 1 CTCVPHPQTAFCSNDLYIRAKFGTPEVNOTTLRYREIKMTKMYKGFQALGDAADIRF 60  
 DB 24 CTCVPHPQTAFCSNDLYIRAKFGTPEVNOTTLRYREIKMTKMYKGFQALGDAADIRF 83  
 QY 61 VYTPMESVCGYFHRSHNRSEEFLLAGKLDGLHITTCSPVAPNNSLSLAQRGFTKTY 120  
 DB 84 IYTPMESVCGYFHRSHNRSEEFLLAGKLDGLHITTCSPVAPNNSLSLAQRGFTKTY 143  
 QY 121 TVGCECTVFPCLSPCKLQSGTHCLMTDQLQSGSEKFGFQSRHLACLPRFGGLCTWQSLR 180  
 DB 144 AAGCECTVFPCLSPCKLQSGTHCLMTDQLQSGSEKFGFQSRHLACLPRFGGLCTWQSLR 203  
 QY 181 SQIA 184  
 DB 204 PRVA 207  
 RESULT 7  
 TIMP1\_HORSE

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ID TIM1_HORSE STANDARD; PRT; 207 AA.
AC O02722;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Metalloproteinase inhibitor 1 precursor (TIMP-1).
GN TIMP1.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cartilage;
RX MEDLINE=99074117; PubMed=9858406;
RA Richardson D.W., Dodge G.R.;
RT "Molecular characteristics of equine stromelysin and the tissue
inhibitor of metalloproteinase 1";
RL Am. J. Vet. Res. 59:1557-1562(1998).
CC -!- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
CC AND IRREVERSIBLY INACTIVATES THEM (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: THE ACTIVITY OF TIMP-1 IS DEPENDENT ON THE PRESENCE OF
CC DISULFIDE BONDS (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE TIMP FAMILY.
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CC -----
DR EMBL; U95039; AAB53735.1; -.
DR HSSP; P01033; LUEA.
DR InterPro; IPR001820; TIMP.
DR Pfam; PF00965; TIMP; 1.
DR SMART; SM00206; TIMP; 1.
DR PROSITE; PS00288; TIMP; 1.
KW Glycoprotein; Metalloprotease inhibitor; Erythrocyte maturation;
KW Signal.
FT CHAIN 1 23 BY SIMILARITY.
FT DISULFID 24 207 METALLOPROTEINASE INHIBITOR 1.
FT DISULFID 24 93 BY SIMILARITY.
FT DISULFID 26 122 BY SIMILARITY.
FT DISULFID 36 147 BY SIMILARITY.
FT DISULFID 150 197 BY SIMILARITY.
FT DISULFID 155 160 BY SIMILARITY.
FT DISULFID 168 189 BY SIMILARITY.
FT DISULFID 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 207 AA; 23046 MW; FD710DA98D168070 CRC64;

Query Match 81.9%; Score 826; DB 1; Length 207;
Best Local Similarity 82.1%; Pred. No. 1.9e-78;
Matches 151; Conservative 12; Mismatches 21; Indels 0; Gaps 0;

Qy 1 CTCVPPHPQTAFCSNDLVIRAKFVGTPEVNTTLYQRYEIKTKMYKGFQALGDAADIRF 60
Db 24 CTCVPPHPQTAFCSSEFVIRAKFVGTSEVNTTLYQRYEIKTKMYKGFQALGDAADIRF 83
Qy 61 VYTPAMESVCGYFHRSHNRSEFLIAGLQDGLHITTCFVAPWNSLSLAQRGFTKTY 120
Db 84 VYTPAMESLCGYFHRSENRESEFLIAGLQDGLHITTCFVAPWNSLSLAQRGFTKTY 143
Qy 121 TVGCECTVFPCLSPCKLQSDTCLWTDQLLGSEKGFQSRHLACLPREPGLCTWQSLR 180
Db 144 AAGCEGCVFPCSSIPCKLQSDTCLWTDQLLGSEKGFQSRHLACLPREPGLCTWQSLR 203
Qy 181 SOIA 184
Db 204 PRTA 207
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RESULT 8
TIM1_RABBIT STANDARD; PRT; 206 AA.
AC P20614;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Metalloproteinase inhibitor 1 precursor (TIMP-1).
GN TIMP1.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89214135; PubMed=2708356;
RA Horowitz S., Dafni N., Shapiro D.L., Holm B.A., Notter R.H.,
RA Quible D.J.;
RT "Hyperoxic exposure alters gene expression in the lung. Induction of
the tissue inhibitor of metalloproteinases mRNA and other mRNAs.";
RL J. Biol. Chem. 264:7092-7095(1989).
CC -!- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
CC AND IRREVERSIBLY INACTIVATES THEM.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: THE ACTIVITY OF TIMP-1 IS DEPENDENT ON THE PRESENCE OF
CC DISULFIDE BONDS.
CC -!- SIMILARITY: BELONGS TO THE TIMP FAMILY.
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CC -----
DR EMBL; J04712; AAA31478.1; -.
DR PIR; A33350; A33350.
DR HSSP; P01033; 1D2B.
DR InterPro; IPR001820; TIMP.
DR Pfam; PF00965; TIMP; 1.
DR SMART; SM00206; TIMP; 1.
DR PROSITE; PS00288; TIMP; 1.
KW Glycoprotein; Metalloprotease inhibitor; Erythrocyte maturation;
KW Signal.
FT CHAIN 1 23 METALLOPROTEINASE INHIBITOR 1.
FT DISULFID 24 206 BY SIMILARITY.
FT DISULFID 26 122 BY SIMILARITY.
FT DISULFID 36 147 BY SIMILARITY.
FT DISULFID 150 196 BY SIMILARITY.
FT DISULFID 155 160 BY SIMILARITY.
FT DISULFID 168 188 BY SIMILARITY.
FT DISULFID 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 206 AA; 22758 MW; 1839A8DE7174EE9E CRC64;

Query Match 81.0%; Score 817.5; DB 1; Length 206;
Best Local Similarity 81.7%; Pred. No. 1.4e-77;
Matches 147; Conservative 11; Mismatches 21; Indels 1; Gaps 1;

Qy 1 CTCVPPHPQTAFCSNDLVIRAKFVGTPEVNTTLYQRYEIKTKMYKGFQALGDAADIRF 60
Db 24 CTCVPPHPQTAFCSNDLVIRAKFVGAPEVNTTLYQRYEIKTKMYKGFQALGDAADIRF 83
Qy 61 VYTPAMESVCGYFHRSHNRSEFLIAGLQDGLHITTCFVAPWNSLSLAQRGFTKTY 120
Db 84 VYTPAMESVCGYSHKSNRSEFLIAGLQDGLHITTCFVAPWNSLSLAQRGFTKTY 143
Qy 121 TVGCECTVFPCLSPCKLQSDTCLWTDQLLGSEKGFQSRHLACLPREPGLCTWQSLR 180
```



Db 144 AAGCMCTVFAACASIPCHLESPTHCLMTDSSL-GSDKGQSHHLACLPOEPGLCMESLR 202

RESULT 9

TIM1\_CANFA STANDARD: PRT: 207 AA.

ID TIM1\_CANFA STANDARD: PRT: 207 AA.

AC P81546; Q9TQ55; 38, Created)

DT 15-JUL-1999 (Rel. 38, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Metalloprotease inhibitor 1 precursor (TIMP-1).

GN TIMP1.

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

OX NCBI\_TaxID=9615;

RN [1]

RP SEQUENCE FROM N.A.

RA STRAIN=MADIN-DURBY;

RA Noritake H., Miyamori H., Goto C., Seiki M., Sato H.;

RL Submitted (AUG-1998) to the EMBL/Genbank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA MEDLINE=99132652; PubMed=9931441;

RA Zeiss C.U., Acland G.M., Aguirre G.D., Ray K.;

RT "TIMP-1 expression is increased in X-linked progressive retinal atrophy despite its exclusion as a candidate gene.;"

RL Gene 225:67-75(1998).

RN [3]

RP CHARACTERIZATION.

RA MEDLINE=92175241; PubMed=1794505;

RA Chopra R., Kokilic P.A., Bergin S., Rowe J., Angel S.;

RT "Purification of recombinant dog tissue inhibitor of metalloproteinases.;"

RL Biochem. Soc. Trans. 19:372S-372S(1991).

CC -1- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES) AND IRREVERSIBLY INACTIVATES THEM.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED. HIGHEST IN KIDNEY AND OVARY.

CC -1- PTM: THE ACTIVITY OF TIMP-1 IS DEPENDENT ON THE PRESENCE OF DISULFIDE BONDS.

CC -1- SIMILARITY: BELONGS TO THE TIMP FAMILY.

CC -----

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CC -----

DR EMBL; AB016817; BAA32393.1; -

DR EMBL; AF077817; AAD10632.1; -

DR EMBL; AF079767; AAD10633.1; -

DR HSSP; P01033; IUBA.

DR InterPro: IPR001820; TIMP.

DR Pfam; PF00965; TIMP.1.

DR SMART; SM00206; TIMP.1.

DR PROSITE; PS00288; TIMP; FALSE\_NEG.

DR GlycoProtein; Metalloprotease inhibitor; Erythrocyte maturation; signal.

KM SIGNAL.

FT CHAIN 1 23 BY SIMILARITY.

FT DISULFID 24 207 METALLOPROTEINASE INHIBITOR 1.

FT DISULFID 26 122 BY SIMILARITY.

FT DISULFID 36 147 BY SIMILARITY.

FT DISULFID 150 197 BY SIMILARITY.

FT DISULFID 155 160 BY SIMILARITY.

FT DISULFID 168 189 BY SIMILARITY.

FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 77 77 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CONFLICT 17 17 V -> L (IN REF. 1).

FT CONFLICT 35 35 L -> F (IN REF. 1).

FT CONFLICT 173 173 H -> Q (IN REF. 1).

FT CONFLICT 203 203 MISSING (IN REF. 1).

SO SEQUENCE 207 AA; 22852 MW; D36C8A67B3B784D CXC64;

Query Match 80.4%; Score 811; DB 1; Length 207;

Best Local Similarity 79.3%; Pred. No. 6,76-77;

Matches 146; Conservative 13; Mismatches 25; Indels 0; Gaps 0;

QY 1 CTCVPPHQTAFCNSDVIYRAKFGVTEPVNOITLYQREIKMTKYKGFQALGDAADIRF 60

Db 24 CTCAPHPQTAFCNSQIVIRAKFVGTAEVNQTDLNRRYEIKMTKMFKGFSAIGNASDIRF 83

QY 61 VTPPMESVCGYFHRSHRSEFFLAGLQDGLHITTCSPFAPNLSLQORRGFTKY 120

Db 84 VDTPALSEYCGILHRSQNRSEFFLVAGNLRDGLINTCSFVAPSSLSSTAQRGFTKY 143

QY 121 TVGCECTVFPCLSIPLCKLQSGTHCLMTDOLQSEKGFQSHHLACLPRPGLCTWQSLR 180

Db 144 AAGCGCTVFTCSSIPCKLQSDPTHCLMTDHLFQTSDKGFQSHHLACLPRPGLCTWQSLR 203

QY 181 SCIA 184

Db 204 PRMA 207

RESULT 10

TIM1\_MOUSE STANDARD: PRT: 205 AA.

ID TIM1\_MOUSE STANDARD: PRT: 205 AA.

AC P12032; P20064;

DT 01-OCT-1989 (Rel. 12, Created)

DT 01-MAY-1991 (Rel. 18, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Metalloprotease inhibitor 1 precursor (TIMP-1) (Erythroid potentiating activity) (EPA) (Tissue inhibitor of metalloproteinases) (Collagenase inhibitor 16C8 fibroblast) (TPA-induced protein) (TPA-SI).

DE (TPA-SI).

GN TIMP1 OR TIMP-1 OR TIMP.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=87218524; PubMed=3034603;

RA Gewert D.R., Coulombe B., Castellino M., Skup D., Williams B.R.G.;

RT "Characterization and expression of a murine gene homologous to human EPA/TIMP: a virus-induced gene in the mouse.;"

RL EMBO J. 6:651-657(1987).

RN [2]

RP SEQUENCE FROM N.A.

RA TISSUE=Fibroblast;

RC MEDLINE=87066763; PubMed=3024122;

RA Edwards D.R., Waterhouse P., Holman M.L., Denhardt D.T.;

RT "A growth-responsive gene (16C8) in normal mouse fibroblasts homologous to a human collagenase inhibitor with erythroid-potentiating activity: evidence for inducible and constitutive transcripts.;"

RL Nucleic Acids Res. 14:8863-8878(1986).

RN [3]

RP SEQUENCE FROM N.A.

RA STRAIN=C3H;

RC MEDLINE=86038821; PubMed=3670294;

RA Johnson M.D., Housey G.M., Kirschmeier P.T., Weinstein I.B.;

RT "Molecular cloning of gene sequences regulated by tumor promoters and mitogens through protein kinase C.;"

RL Mol. Cell. Biol. 7:2821-2829(1987).

CC -1- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES) AND IRREVERSIBLY INACTIVATES THEM. ALSO MEDIATES ERYTHROPOIETIS IN VITRO; BUT, UNLIKE IL-3, IT IS SPECIES-SPECIFIC, STIMULATING THE GROWTH AND DIFFERENTIATION OF ONLY HUMAN AND MURINE ERYTHROID PROGENITORS.

CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: FOUND IN FETAL AND ADULT TISSUES. HIGHEST  
CC LEVELS ARE FOUND IN BONE. ALSO FOUND IN LUNG, OVARY AND UTERUS.  
CC -1- INDUCTION: REGULATED BY TUMOR PROMOTERS AND MITOGENS THROUGH  
CC PROTEIN KINASE C. ALSO INDUCED BY VIRUSES.  
CC -1- PTM: THE ACTIVITY OF TIMP-1 IS DEPENDENT ON THE PRESENCE OF  
CC DISULFIDE BONDS.  
CC -1- SIMILARITY: BELONGS TO THE TIMP FAMILY.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; M28312; AAB42179.1; -  
CC EMBL; M28308; AAB42179.1; JOINED.  
CC EMBL; M28309; AAB42179.1; JOINED.  
CC EMBL; M28310; AAB42179.1; JOINED.  
CC EMBL; M28311; AAB42179.1; JOINED.  
CC EMBL; X04684; CAA28387.1; -  
CC EMBL; M17243; AAB40471.1; -  
CC PIR; A26633; A26633.  
CC PIR; A26106; A26106.  
CC PIR; A26917; A26917.  
CC HSP; P01033; 1UEA.  
CC MGD; MGI:98752; Timp.  
CC InterPro; IPR001820; TIMP.  
CC Pfam; PF00965; TIMP; 1.  
CC SMART; SM00206; TIMP; 1.  
CC PROSITE; PS00288; TIMP; 1.  
CC Glycoprotein; Metalloprotease inhibitor; Erythrocyte maturation;  
CC KW  
CC Signal.  
CC  
CC CHAIN 1 24 METALLOPROTEINASE INHIBITOR 1.  
CC FT CHAIN 25 205  
CC FT DISULFID 25 94 BY SIMILARITY.  
CC FT DISULFID 27 123 BY SIMILARITY.  
CC FT DISULFID 37 148 BY SIMILARITY.  
CC FT DISULFID 151 197 BY SIMILARITY.  
CC FT DISULFID 156 161 BY SIMILARITY.  
CC FT DISULFID 169 189 BY SIMILARITY.  
CC FT CARBOHYD 54 54 N-LINKED (GLCNAC. .) (POTENTIAL).  
CC FT CARBOHYD 102 102 N-LINKED (GLCNAC. .) (POTENTIAL).  
CC FT CONFLICT 52 52 E -> R (IN REF. 1).  
CC FT CONFLICT 66 66 M -> MM (IN REF. 1).  
CC FT CONFLICT 117 118 NL -> KF (IN REF. 1).  
CC FT CONFLICT 121 121 S -> N (IN REF. 1).  
CC FT CONFLICT 139 139 A -> V (IN REF. 1).  
CC FT CONFLICT 143 143 T -> KN (IN REF. 1).  
CC FT CONFLICT 194 194 P -> L (IN REF. 1).  
CC SEQUENCE 205 AA; 22628 MW; FACA952D49A50FD7 CRC64;  
Query Match 75.5%; Score 761.5; DB 1; Length 205;  
Best Local Similarity 73.7%; Pred. No. 9e-72;  
Matches 132; Conservative 25; Mismatches 21; Indels 1; Gaps 1;  
Qy 1 CTCVPHPTACNSDLVIRAKFVGTPEVNOTTLVORVEIKMTKMYKGFOALGDAADIRF 60  
Db 25 CSCAPHPPTACNSDLVIRAKFVGTPEVNOTTLVORVEIKMTKMYKGFOALGDAADIRF 84  
Qy 61 VYTPAMESVCGYFHRSHNRSEBFLIAGLQDLGLHITTCSPVAPNLSLAQRGGFTKTY 120  
Db 85 AYTPTWESLCGYAHKSNQSEBFLITGLRNLGNLHISACSLFVPTLTSPAQRAFSTKY 144  
Qy 121 TVGCECTVFPCLSPCKLQSTHCLWTDLQLOGSEKGFQSHLACLPREPGLCWTQSL 179  
Db 145 SAGCGVCTVFPCLSPCKLESHTCLWTDLQVLVSGE-DYQSRHFACLPENPLGCTWRS 202  
RESULT 11  
TIMP\_RAT

107 RAT STANDARD; PRT; 217 AA.  
AC P0120; P70533;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Metalloprotease inhibitor 1 precursor (TIMP-1).  
GN TIMP1 OR TIMP-1.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RN SEQUENCE FROM N.A.  
RN STRAIN=Wistar; TISSUE=Skin dorsal;  
RX MEDLINE=95011636; PubMed=7926820;  
RA Okada A., Garnier J.M., Vicaire S., Basset P.;  
RT "Cloning of the cDNA encoding rat tissue inhibitor of  
RT metalloproteinase 1 (TIMP-1), amino acid comparison with other TIMPs,  
RT and gene expression in rat tissues.";  
RL Gene 147:301-302(1994).  
RN [2]  
RN SEQUENCE FROM N.A.  
RN TISSUE=Mammary gland;  
RA Gibbons K.L., O'Grady R.L., Piper A.A.;  
RT Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RN SEQUENCE OF 30-205 FROM N.A.  
RN TISSUE=Liver;  
RX MEDLINE=96317624; PubMed=8707259;  
RA Iredale J.P., Benyon R.C., Arthur M.J.P., Ferris W.F., Alcolado R.,  
RA Winwood P.J., Clark N., Murphy G.;  
RT "Tissue inhibitor of metalloproteinase-1 messenger RNA expression is  
RT enhanced relative to interstitial collagenase messenger RNA in  
RT experimental liver injury and fibrosis.";  
RL Hepatology 24:176-184(1996).  
RN [4]  
RN SEQUENCE OF 39-156 FROM N.A., SEQUENCE OF 24-38, INDUCTION, FUNCTION,  
RN AND SUBCELLULAR LOCATION.  
RX STRAIN=Sprague-Dawley; TISSUE=Sertoli cells;  
RX MEDLINE=95296691; PubMed=777858;  
RA Boujrad N., Ogwegbu S.O., Garnier M., Lee C.-H., Martin B.M.,  
RA Papadopoulos V.;  
RT "Identification of a stimulator of steroid hormone synthesis isolated  
RT from testis.";  
RL Science 268:1609-1612(1995).  
RN [5]  
RN SEQUENCE OF 24-45.  
RX MEDLINE=92117648; PubMed=1309971;  
RA Roswit W.T., McCourt D.W., Partridge N.C., Jeffrey J.J.;  
RT "Purification and sequence analysis of two rat tissue inhibitors of  
RT metalloproteinases.";  
RL Arch. Biochem. Biophys. 292:402-410(1992).  
CC -1- FUNCTION: Complexes with metalloproteinases (such as collagenases)  
CC and irreversibly inactivates them. Also stimulates steroidogenesis  
CC by Leydig and ovarian granulosa cells; procathepsin L is required  
CC for maximal activity.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- INDUCTION: By follicle-stimulating hormone (FSH).  
CC -1- PTM: THE ACTIVITY OF TIMP-1 IS DEPENDENT ON THE PRESENCE OF  
CC DISULFIDE BONDS.  
CC -1- SIMILARITY: BELONGS TO THE TIMP FAMILY.  
CC  
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CC  
CC EMBL; U06179; AAA85780.1; -  
CC EMBL; L31883; AAA85373.1; -  
CC EMBL; L29512; AAB08483.1; -

DR EMBL; U16022; AAA51653.1; ALT\_SEQ.  
 DR PIR; S20326; S20326.  
 DR HSSP; P01033; IUEA.  
 DR InterPro; IPR001820; TIMP.  
 DR Pfam; PF00965; TIMP; 1.  
 DR SMART; SM00206; TIMP; 1.  
 DR PROSITE; PS00288; TIMP; 1.  
 DR Glycoprotein; Metalloprotease inhibitor; Erythrocyte maturation;  
 KW Steroidogenesis; Signal.  
 FT SIGNAL 1 23  
 FT CHAIN 24 217 METALLOPROTEINASE INHIBITOR 1.  
 FT DISULFID 24 93 BY SIMILARITY.  
 FT DISULFID 26 122 BY SIMILARITY.  
 FT DISULFID 36 147 BY SIMILARITY.  
 FT DISULFID 150 197 BY SIMILARITY.  
 FT DISULFID 155 160 BY SIMILARITY.  
 FT DISULFID 168 189 BY SIMILARITY.  
 FT CARBOHYD 77 77 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 80 81 GP -> DI (IN REF. 3).  
 FT CONFLICT 88 88 A -> V (IN REF. 4).  
 FT CONFLICT 103 103 S -> R (IN REF. 3).  
 FT CONFLICT 129 130 HN -> AS (IN REF. 3).  
 FT CONFLICT 136 140 OKAFV -> RKGLT (IN REF. 3).  
 FT CONFLICT 149 149 V -> L (IN REF. 4).  
 FT CONFLICT 157 157 S -> V (IN REF. 3).  
 FT CONFLICT 166 166 A -> T (IN REF. 3).  
 FT CONFLICT 185 187 DHF -> RHL (IN REF. 3).  
 FT CONFLICT 195 195 D -> G (IN REF. 3).  
 FT CONFLICT 201 201 Y -> S (IN REF. 3).  
 FT CONFLICT 204 205 VS -> SR (IN REF. 3).  
 FT SEQUENCE 217 AA; 23793 MW; C5AC240A61C1A1DF CRC64;

Query Match 73.5%; Score 742; DB 1; Length 217;  
 Best Local Similarity 71.5%; Pred. No. 1e-69;  
 Matches 128; Conservative 23; Mismatches 28; Indels 0; Gaps 0;

QY 1 CTCVPPHPOTACNSDLYIRAKFVGTPEVNOFTL-YQRYEIKMTKWKYKGFQALGDADIRF 60  
 DB 24 CSCAPHPPTACNSDLYIRAKFMSPEIETTLVQRYEIKMTKMKGFDVGNATGFRF 83  
 QY 61 YVTPEMSVQGYFHRSHNSEEFLLAGKLQDGLHITTCGFVAPWNSLSLAQRGFTKT 120  
 DB 84 AYTPAMESLCGYVHKSQNSEEFLLAGRLRNGLHITTACSPFLVPMNLBPAAQKAFVKTY 143  
 QY 121 YTGCECTVFPCLSIPTCKLQSGTHCLMTDQLLOGSEKGFQSRHLACLPRPGLCTWQSL 179  
 DB 144 SAGCGVCTVFPCLSIPTCKLQSGTHCLMTDQILMGSEKGYQSDHFACTLPNNPDLCTWQYL 202  
 RESULT 12  
 TIM3\_SCYTO  
 ID TIM3\_SCYTO STANDARD; PRT; 214 AA.  
 AC Q9W6B4;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Metalloprotease inhibitor 3 precursor (TIMP-3) (Tissue inhibitor of  
 DE metalloproteases-3).  
 GN TIMP3.  
 OS Scyliorhinus torazame (Cloudy catshark).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
 OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;  
 OC Scyliorhinidae; Scyliorhinus.  
 OC NCBI\_TaxID=75743;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Cartilage;  
 RX PubMed=11342115;  
 RA Kim J.-T., Kim M.-S., Bae M.-K., Song H.S., Ahn M.-Y., Kim Y.-J.,  
 RA Lee S.-J., Kim K.-W.,  
 RA "Cloning and characterization of tissue inhibitor of  
 RT metalloprotease-3 (TIMP-3) from shark, Scyliorhinus torazame.";

RL Biochim. Biophys. Acta 1517:311-315 (2001).  
 CC -!- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)  
 CC AND IRREVERSIBLY INACTIVATES THEM. MAY FORM PART OF A TISSUE-  
 CC SPECIFIC ACUTE RESPONSE TO REMODELING STIMULI (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Secreted. Extracellular matrix (By  
 CC similarity).  
 CC -!- TISSUE SPECIFICITY: Expressed abundantly in brain and cartilage.  
 CC -!- SIMILARITY: BELONGS TO THE TIMP FAMILY.  
 CC -----  
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 CC -----

DR EMBL; AF110767; AAD26150.1; .  
 DR HSSP; P16035; 2TMP.  
 DR InterPro; IPR001820; TIMP.  
 DR Pfam; PF00965; TIMP; 1.  
 DR SMART; SM00206; TIMP; 1.  
 DR PROSITE; PS00288; TIMP; 1.  
 DR Metalloprotease inhibitor; Signal.  
 FT SIGNAL 1 26  
 FT CHAIN 27 214 METALLOPROTEINASE INHIBITOR 3.  
 FT DISULFID 27 94 BY SIMILARITY.  
 FT DISULFID 29 121 BY SIMILARITY.  
 FT DISULFID 39 146 BY SIMILARITY.  
 FT DISULFID 148 195 BY SIMILARITY.  
 FT DISULFID 153 158 BY SIMILARITY.  
 FT DISULFID 166 187 BY SIMILARITY.  
 FT CARBOHYD 210 210 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT SEQUENCE 214 AA; 24498 MW; BCAD3008BE48357 CRC64;

Query Match 38.5%; Score 388.5; DB 1; Length 214;  
 Best Local Similarity 40.1%; Pred. No. 4.4e-33;  
 Matches 71; Conservative 32; Mismatches 67; Indels 7; Gaps 4;

QY 1 CTCVPPHPOTACNSDLYIRAKFVGTPEVNOFTL-YQRYEIKMTKWKYKGFQALGDADIR 59  
 DB 27 CTCWNNHPOEAFNCNSDIVIRAKVWGKLLKDPFGTMRYYTLKOMMYGKFGSKM--QQVQ 83  
 QY 60 FYVTPEMSVQGYFHRSHNSEEFLLAGKLQDGLHITTCGFVAPWNSLSLAQRGFTKT 119  
 DB 84 YITPEASLQGV--RLQVNFQYLTGRVDFGEVYTCVNFVPMWDLTUSQKGLNHR 141  
 QY 120 YTGCECTVFPCLSIPTCKLQSGTHCLMTDQLLOGSEKGFQSRHLACLPRPGLCTW 176  
 DB 142 YQYGC-NCKIKRCYLLPCFVTAKNCEFTMDLSDQGVNGHAKYVVCIRQKRGYCSW 197

RESULT 13  
 TIM2\_CHICK  
 ID TIM2\_CHICK STANDARD; PRT; 220 AA.  
 AC O42146;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Metalloprotease inhibitor 2 precursor (TIMP-2) (Tissue inhibitor of  
 DE metalloproteases-2).  
 GN TIMP2.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauiria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OC NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=96122528; PubMed=9462696;  
 RX Aimes R.T., Li L.H., Weaver B., Hawkes S., Hahn-Dantona E.A.,  
 RA Outgley J.P.;  
 RA "Cloning, expression, and characterization of chicken tissue

```

RT inhibitor of metalloproteinase-2 (TIMP-2) in normal and transformed
RT chicken embryo fibroblasts."
RL J. Cell. Physiol. 174:342-352(1998).
CC -!- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
CC AND IRREVERSIBLY INACTIVATES THEM (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PFM: THE ACTIVITY OF TIMP-2 IS DEPENDENT ON THE PRESENCE OF
CC DISULFIDE BONDS.
CC -!- SIMILARITY: BELONGS TO THE TIMP FAMILY.
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CC -----
CC EMBL; AF004664; AAB69168.1; -.
CC HSP; P16035; 2TMP.
CC InterPro; IPR001820; TIMP.
CC Pfam; PF00965; TIMP; 1.
CC SMART; SM00206; TIMP; 1.
CC PROSITE; PS00288; TIMP; 1.
CC Metalloprotease inhibitor; Signal.
FT SIGNAL 1 26
FT CHAIN 27 220 METALLOPROTEINASE INHIBITOR 2.
FT DISULFID 27 98 BY SIMILARITY.
FT DISULFID 29 127 BY SIMILARITY.
FT DISULFID 39 152 BY SIMILARITY.
FT DISULFID 154 201 BY SIMILARITY.
FT DISULFID 159 164 BY SIMILARITY.
FT DISULFID 172 193 BY SIMILARITY.
SQ SEQUENCE 220 AA; 61BDAC760B752E53 CRC64;

Query Match 38.0%; Score 383.5; DB 1; Length 220;
Best Local Similarity 42.9%; Pred. No. 1.5e-32;
Matches 79; Conservative 26; Mismatches 64; Indels 15; Gaps 6;

QY 1 CTCVPPHPTAFCSNLDLVIKAFVGTPEVNO-TTLVQ-----RYEIKWTQMYKGFQALG 53
DB 27 CSCSIHPQAFQCNADVIRAKVSEKVDGNDIYGNPIKRIQYEVKQIMFK-----G 81

QY 54 DAADIRFVYTPAMESVCGYFHRSHNRSEFLIAGKLQ-DGLLHITTCFVAPWNSLSLAQ 112
DB 82 PQDIEFIYTPSTVCGQ-PLDTGCKEYLIAGKSEGDKGKHITLCDLVATWDSVPTQ 140

QY 113 RRGFTKTYTVGCECTVFPCLSPCKLQSGTHCLWTDQLLOGSEKGFQSRHLACLPRPG 172
DB 141 KKLNLQRYQMG-C-EKISRCLSPCFVSSSDECLWTDWAMEKIVGGQKQHVACIKRSDG 199

QY 173 LCTW 176
DB 200 SCAM 203

RESULT 14
TIM2 MOUSE
ID TIM2 MOUSE STANDARD; PRT; 220 AA.
AC P25785;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Metalloprotease inhibitor 2 precursor (TIMP-2) (Tissue inhibitor of
DE metalloproteinase-2).
GN TIMP2 OR TIMP-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=BAUB/c;

```

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RX MEDLINE=92290292; PubMed=1601312;
RA Shimizu S., Malik K., Sejima H., Kishi J.I., Hayakawa T., Koiwai O.;
RT "Cloning and sequencing of the cDNA encoding a mouse tissue inhibitor
RT of metalloproteinase-2."
RL Gene 114:291-292(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92347695; PubMed=1639268;
RA Leco K.J., Hayden L.J., Sharma R.R., Rocheleau H., Greenberg A.H.,
RA Edwards D.R.;
RT "Differential regulation of TIMP-1 and TIMP-2 mRNA expression in
RT normal and Ha-ras-transformed murine fibroblasts."
RL Gene 117:209-217(1992).
RN [3]
RP PRELIMINARY SEQUENCE OF 27-62.
RX MEDLINE=91226375; PubMed=1851244;
RA Kishi J.I., Ogawa K., Yamamoto S., Hayakawa T.;
RT "Purification and characterization of a new tissue inhibitor of
RT metalloproteinases (TIMP-2) from mouse colon 26 tumor cells."
RL Matrix 11:10-16(1991).
CC -!- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
CC AND IRREVERSIBLY INACTIVATES THEM.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PFM: THE ACTIVITY OF TIMP-2 IS DEPENDENT ON THE PRESENCE OF
CC DISULFIDE BONDS.
CC -!- SIMILARITY: BELONGS TO THE TIMP FAMILY.
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CC -----
CC EMBL; X62622; CAA44491.1; -.
CC EMBL; M82858; AAA40445.1; -.
CC EMBL; M93954; AAA40446.1; -.
CC PIR; S15987; S15987.
CC PIR; JH0683; JH0683.
CC HSP; P16035; IBR9.
CC MCD; MGI:98753; Timp2.
CC InterPro; IPR001820; TIMP.
CC Pfam; PF00965; TIMP; 1.
CC SMART; SM00206; TIMP; 1.
CC PROSITE; PS00288; TIMP; 1.
CC Metalloprotease inhibitor; Signal.
FT SIGNAL 1 26
FT CHAIN 27 220 METALLOPROTEINASE INHIBITOR 2.
FT DISULFID 27 98 BY SIMILARITY.
FT DISULFID 29 127 BY SIMILARITY.
FT DISULFID 39 152 BY SIMILARITY.
FT DISULFID 154 201 BY SIMILARITY.
FT DISULFID 159 164 BY SIMILARITY.
FT DISULFID 172 193 BY SIMILARITY.
FT CONFLICT 12 12 L -> H (IN REF. 2).
FT CONFLICT 21 21 V -> L (IN REF. 2).
FT CONFLICT 195 195 K -> E (IN REF. 2).
SQ SEQUENCE 220 AA; 1D0A16CEDA023F0D CRC64;

Query Match 37.9%; Score 382.5; DB 1; Length 220;
Best Local Similarity 41.8%; Pred. No. 1.9e-32;
Matches 77; Conservative 27; Mismatches 65; Indels 15; Gaps 6;

QY 1 CTCVPPHPTAFCSNLDLVIKAFVGTPEVNO-TTLVQ-----RYEIKWTQMYKGFQALG 53
DB 27 CSCSIHPQAFQCNADVIRAKVSEKVDGNDIYGNPIKRIQYEVKQIMFK-----G 81

QY 54 DAADIRFVYTPAMESVCGYFHRSHNRSEFLIAGKLQ-DGLLHITTCFVAPWNSLSLAQ 112
DB 82 PQDIEFIYTPSSAVCG-VSLDVGKKEYLIAGKSEGDKGKHITLCDLVATWDTLSITQ 140

QY 113 RRGFTKTYTVGCECTVFPCLSPCKLQSGTHCLWTDQLLOGSEKGFQSRHLACLPRPG 172

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Db 141 KSLNHRQMG-C-ECKITRCPMIPYISSPDECLMMDWTEKSIHQAKFPACIKRSDG 199
Oy 173 LCTW 176
Db 200 SCAM 203

RESULT 15
TIM2_RAT ID TIM2_RAT STANDARD; PRT; 220 AA.
AC P30121.
DT 01-APR-1993 (Rel. 25, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Metalloproteinase inhibitor 2 precursor (TIMP-2) (Tissue inhibitor of
DE metalloproteinases-2).
GN TIMP2 OR TIMP-2.
OC Rattus norvegicus (Rat).
OC Sukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Bone;
RX MEDLINE=94263207; PubMed=8203893;
RA Cook T.F., Burke J.S., Bergman K.D., Quinn C.O., Jeffrey J.J.,
RA Partridge N.C.;
RT "Cloning and regulation of rat tissue inhibitor of
RT metalloproteinases-2 in osteoblastic cells."
RL Arch. Biochem. Biophys. 311:313-320(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Gibbons K.L., O'Grady R.L., Piper A.A.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=94326839; PubMed=8050496;
RA Sanctoro M., Battaglia C., Zhang L., Carlomagno F., Martelli M.L.,
RA Salvatore D., Fusco A.;
RT "Cloning of the rat tissue inhibitor of metalloproteinases type 2
RT (TIMP-2) gene: analysis of its expression in normal and transformed
RT thyroid cells."
RL Exp. Cell Res. 213:398-403(1994).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=96384329; PubMed=8792217;
RA Grima J., Calcagno K., Cheng C.Y.;
RT "Purification, cDNA cloning, and developmental changes in the steady-
RT state mRNA level of rat testicular tissue inhibitor of
RT metalloproteinases-2 (TIMP-2)."
RL J. Androl. 17:263-275(1996).
RN [5]
RP SEQUENCE OF 27-48.
RX MEDLINE=92117648; PubMed=1309971;
RA Roswit W.T., McCourt D.W., Partridge N.C., Jeffrey J.J.;
RT "Purification and sequence analysis of two rat tissue inhibitors of
RT metalloproteinases."
RL Arch. Biochem. Biophys. 292:402-410(1992).
CC -1- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
CC AND IRREVERSIBLY INACTIVATES THEM.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: THE ACTIVITY OF TIMP-2 IS DEPENDENT ON THE PRESENCE OF
CC -1- DISULFIDE BONDS.
CC -1- SIMILARITY: BELONGS TO THE TIMP FAMILY.
CC -----
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CC -----
DR EMBL: U14526; AAA21553.1; -
DR EMBL: L31884; AAA84581.1; -
DR EMBL: S72594; AAC60687.1; -
DR EMBL: S82718; AAB49507.1; -
DR PIR: S20325; S20325.
DR HSSP: P16035; 1BR9.
DR InterPro: IPR001820; TIMP.
DR Pfam: PF00965; TIMP.1.
DR SMART: SM00206; TIMP.1.
DR PROSITE: PS00288; TIMP.1.
KW Metalloproteinase inhibitor; Signal.
FT SIGNAL 1 26
FT CHAIN 27 220 METALLOPROTEINASE INHIBITOR 2.
FT DISULFID 27 98 BY SIMILARITY.
FT DISULFID 29 127 BY SIMILARITY.
FT DISULFID 39 152 BY SIMILARITY.
FT DISULFID 154 201 BY SIMILARITY.
FT DISULFID 159 164 BY SIMILARITY.
FT DISULFID 172 193 BY SIMILARITY.
FT CONFLICT 7 7 S -> T (IN REF. 1).
FT CONFLICT 153 153 E -> Q (IN REF. 1).
SQ SEQUENCE 220 AA; 24356 MW; 1C97A3F050C3AETD CRC64;

Query Match 37.9%; Score 382.5; DB 1; Length 220;
Best Local Similarity 41.8%; Pred. No. 1.9e-32;
Matches 77; Conservative 27; Mismatches 65; Indels 15; Gaps 6;

Oy 1 CTCVPHHPQTAFCNSDLVIRAKFVGTPEVNO-TTLVQ-----RYEIKMTKMYKGFQALG 53
Db 27 CSCSPVHPQAFQCNADVIRAKAVEKEVDGNDYGNPIRIQYEIKQIKFK-----G 81
Oy 54 DAADIRFVYTPAMESVCGYFHRSHNRSEFLIAGKQ-DGLHITTCSPVAPWNSLSLAQ 112
Db 82 PDKDIEFLYTPASSAVCG-VSLDVGKKKEYLIAGKAEQDGKMHITLCPFIWMDLSITQ 140
Oy 113 RRGFTKTVTGCEETVPPCLSPCKLQSGTHCLWTDLLQSGSEKGFQSRHLACLPBPG 172
Db 141 KSLNHRQMG-C-ECKITRCPMIPYISSPDECLMMDWTEKSIHQAKFPACIKRSDG 199
Oy 173 LCTW 176
Db 200 SCAM 203

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Search completed: December 17, 2002, 15:04:52  
Job time : 11.1517 secs

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OM protein - protein search, using sw model

Run on: December 17, 2002, 15:04:31 ; Search time 33.6276 Seconds  
(without alignments)  
1127.428 Million cell updates/sec

Title: US-09-452-817-1

Perfect score: 1009  
Sequence: 1 CTCVPHPHQTAFCNSDLVIR.....ACLPREPGLCTWQSLRSQIA 184

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Sequences: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_21:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mmc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_protist:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	800	79.3	169 4	Q96QM2
2	633	62.7	137 6	Q9M212
3	515	51.0	145 11	Q912P7
4	368.5	36.5	194 11	Q92506
5	297.5	29.5	152 6	Q9T7B7
6	282	27.9	170 6	Q9T7B6
7	246.5	24.4	138 6	Q9T7B8
8	232.5	23.0	126 6	Q95KL7
9	188.5	18.7	97 6	Q95KL8
10	181.5	18.0	221 11	Q96PJ2
11	149.5	14.8	38 11	Q61720
12	129.5	12.8	97 13	Q8UWZ2
13	124	12.3	25 11	Q9QUW9
14	124	12.3	25 11	Q9QV13
15	106.5	10.6	280 5	Q962H0
16	106	10.5	30 11	Q9QV14

17	88.5	8.8	512	11	Q9DAQ1	Q9daq1 mus musculu
18	83.5	8.3	187	5	Q9NDF1	Q9ndf1 heterodera
19	83	8.2	4307	5	Q19319	Q19319 caenorhabdi
20	79.5	7.9	1062	5	Q19204	Q19204 caenorhabdi
21	79	7.8	682	10	Q9LTF3	Q9ltf3 arabidopsis
22	77.5	7.7	701	11	Q9ZJ12	Q9zj12 mus musculu
23	76.5	7.6	626	10	Q9FXY0	Q9fxy0 arabidopsis
24	76	7.5	340	3	Q9P3W4	Q9p3w4 schizosacch
25	75.5	7.5	257	16	Q9J2H6	Q9j2h6 staphylococ
26	75.5	7.5	530	10	Q80793	Q80793 arabidopsis
27	75.5	7.5	1106	13	Q42291	Q42291 gallus gall
28	75.5	7.5	1513	11	Q62635	Q62635 rattus norv
29	74.5	7.4	263	10	Q9AVH5	Q9avh5 pistum sativ
30	74.5	7.4	444	11	Q91W22	Q91w22 mus musculu
31	74.5	7.4	1326	4	Q9P219	Q9p219 homo sapien
32	74	7.3	158	5	Q21265	Q21265 caenorhabdi
33	74	7.3	1006	12	Q85064	Q85064 peanut stun
34	74	7.3	1179	5	Q9NBM4	Q9nbm4 trypanosoma
35	73.5	7.3	444	4	Q9GZ57	Q9gz57 homo sapien
36	73.5	7.3	1963	4	Q75051	Q75051 homo sapien
37	73	7.2	555	10	Q23590	Q23590 arabidopsis
38	73	7.2	993	12	Q8UYT4	Q8uyt4 tomato aspe
39	73	7.2	3132	12	Q9QW08	Q9qwo8 japanese ya
40	72.5	7.2	225	5	Q27013	Q27013 tenedrio mo
41	72.5	7.2	225	5	Q27014	Q27014 tenedrio mo
42	72.5	7.2	425	12	Q68393	Q68393 human cytom
43	72.5	7.2	517	4	Q75294	Q75294 homo sapien
44	72.5	7.2	611	16	Q9KAS8	Q9kas8 bacillus ha
45	72	7.1	109	4	Q13058	Q13058 homo sapien

## ALIGNMENTS

## RESULT 1

Q96QM2 PRELIMINARY: PRT: 169 AA.

AC Q96QM2: 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

DE Tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

NCBI\_taxid=9606;

NCBI [1]

SEQUENCE FROM N.A.

RC TISSUE=PROSTATE;

RA Straubeberg R.;

RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: BC007097; AAH07097.1; -

DR InterPro: IPR001820; TIMP.

DR Pfam: PF00965; TIMP.1.

DR PROSITE: PS00288; TIMP. UNKNOWN 1.

DR SEQUENCE 169 AA; 18847 MW; EC164206C87D815C CRC64;

Query Match 79.3%; Score 800; DB 4; Length 169;  
Best local Similarity 100.0%; Pred. No. 8e-80;  
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CTCVPHPHQTAFCNSDLVIRAKFVGTPVNOITLYORREIKMTKYKGFOLGDAADIRF	60
DB	24	CTCVPHPHQTAFCNSDLVIRAKFVGTPVNOITLYORREIKMTKYKGFOLGDAADIRF	83
QY	61	VYTPMSEVCGYFHRSHRSEEFILAGKLQDGLHITTCSEFVAPWNSLSLQRRGFTYTY	120
DB	84	VYTPMSEVCGYFHRSHRSEEFILAGKLQDGLHITTCSEFVAPWNSLSLQRRGFTYTY	143
QY	121	TVGCECTVFPCLSTPCKLQSGTHCL	146
DB	144	TVGCECTVFPCLSTPCKLQSGTHCL	169

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RESULT 2
Q9WZ12
ID Q9WZ12 PRELIMINARY; PRT; 137 AA.
AC Q9WZ12;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Tissue inhibitor of metalloproteinase 1 (Fragment).
GN TIMP1.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20347710; PubMed=10888873;
RA Galloway S.M., McNatty K.P., Cambridge L.M., Laitinen M.P.E.,
RA Juengel J.L., Jokiranta S., McLaren R.J., Luiro K., Dodds K.D.,
RA Montgomery G.W., Beattie A.E., Davis G.H., Ritvos O.;
RA "Mutations in an oocyte-derived growth factor (BMP15) cause increased
RT ovulation rate and infertility in a dosage-sensitive manner.";
RL Nat. Genet. 25:279-283(2000).
DR EMBL; AF268477; AAF81746.1; -.
DR HSSP; P01033; 1D2B.
DR InterPro; IPR001820; TIMP.
DR Pfam; PF00965; TIMP; 1.
DR SMART; SM00206; TIMP; 1.
FT NON_TER 1
FT NON_TER 137
SQ SEQUENCE 137 AA; 15396 MW; 62009B069D0594B7 CRC64;

Query Match 62.7%; Score 633; DB 6; Length 137;
Best Local Similarity 84.7%; Pred. No. 1.3e-61;
Matches 116; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

QY 7 HPQAFCSNLDVIRAKFVGTPVNO-TTLVQ-----RYEIKMTKMYKGFQALG 66
DB 1 HPQAFCSNLDVIRAKFVGTPVNO-TTLVQ-----RYEIKMTKMYKGFQALG 66
QY 67 ESVCCGYEHRSHNRSEEFLLAGLQGLLHITTCFVAPWNSLSLAORRGFTKTYVGCEE 126
DB 61 ESVCCGYEHRSHNRSEEFLLAGLQGLLHITTCFVAPWNSLSLAORRGFTKTYAAGCEE 120
QY 127 CTVFPCLSPCKLQSGT 143
DB 121 CTVFPCLSPCKLQSGT 137

RESULT 3
Q91ZP7
ID Q91ZP7 PRELIMINARY; PRT; 145 AA.
AC Q91ZP7;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Tissue inhibitor of metalloproteinase 1 (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR; TISSUE=OVARY;
RA Espey L.L., Ujioka T., Okamura H., Richards J.S.;
RT "Expression of metallothionein-1 (MT-1) in steroid-secreting cells of
RT the rat ovary during the peri-ovulatory period following gonadotropin
RT treatment.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF411319; AAL05862.1; -.
DR InterPro; IPR001820; TIMP.
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DR Pfam; PF00965; TIMP; 1.
FT NON_TER 1
SQ SEQUENCE 145 AA; 15954 MW; 7EC7053DA82DE913 CRC64;

Query Match 51.0%; Score 515; DB 11; Length 145;
Best Local Similarity 68.2%; Pred. No. 1.3e-48;
Matches 88; Conservative 18; Mismatches 23; Indels 0; Gaps 0;

QY 51 ALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLLAGLQGLLHITTCFVAPWNSLSL 110
DB 2 AVGNATGFRAYTPAMESLCGYVHKSQNRSEEFLLAGLQGLLHITTCFVAPWNSLSL 61
QY 111 AORRGFTKTYVGCEECTVFPCLSPCKLQGLHITTCFVAPWNSLSLAORRGFTKTYVGCEE 170
DB 62 AQQKAFVKTYSAGCGVCTVFPCLSPCKLQGLHITTCFVAPWNSLSLAORRGFTKTYVGCEE 121
QY 171 PGLCTWQSL 179
DB 122 PDLCTWQYL 130

RESULT 4
Q925Q6
ID Q925Q6 PRELIMINARY; PRT; 194 AA.
AC Q925Q6;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Tissue inhibitor of matrix metalloproteinase-2 (Fragment).
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RA Ko K.H., Shin C.Y., Lee W.J., Yoo B.K., Ryu J.R., Park K.H.;
RT "Expression of metalloproteinase-2 (gelatinase A) and tissue inhibitor
RT of metalloproteinase-2 (TIMP-2) from hamster tracheal goblet cells: a
RT possible role in upper airway inflammation.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF260255; AAK51636.1; -.
DR InterPro; IPR001820; TIMP.
DR Pfam; PF00965; TIMP; 1.
FT NON_TER 1
FT NON_TER 194
SQ SEQUENCE 194 AA; 21763 MW; 1C5D10A3D38A8941 CRC64;

Query Match 36.5%; Score 368.5; DB 11; Length 194;
Best Local Similarity 40.8%; Pred. No. 2.2e-32;
Matches 75; Conservative 27; Mismatches 67; Indels 15; Gaps 6;

QY 1 CTCVPPHPQAFCSNLDVIRAKFVGTPVNO-TTLVQ-----RYEIKMTKMYKGFQALG 53
DB 1 CSCSPVHQQAFCNADVVIRAKVSEKVDGNDIYGNPKVRIQYIEIKQIMFK-----G 55
QY 54 DAADIRFVYTPAMESVCGYFHRSHNRSEEFLLAGLQGLLHITTCFVAPWNSLSLAQ 112
DB 56 PKDIEFTYTPASSAMCG-VSLDVGKKEVLIAGKAGDGKWHITLCLDFIVPMDTLSTTQ 114
QY 113 RRGFTKTYVGCEECTVFPCLSPCKLQGLHITTCFVAPWNSLSLAORRGFTKTYVGCEE 172
DB 115 KSLNHRHYQMGCECKITRCMPICYSIPSSPDECLWMDWVTEKSIHQHQAFFACIKRSDG 173
QY 173 LCTW 176
DB 174 SCW 177

RESULT 5
Q9TTB7
ID Q9TTB7 PRELIMINARY; PRT; 152 AA.
AC Q9TTB7;
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DT 01-MAY-2000 (Tremblrel. 13, Created)  
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
 DE Metalloproteinase inhibitor 3 (TIMP-3) (Tissue inhibitor of metalloproteinase-3) (Fragment).  
 GN TIMP-3.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Wang J.F., Boykiw R.H., Reno C.R., Hart D.A., Olson M.E.;  
 RT "Cloning and sequencing of porcine TIMPs."  
 RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.  
 CC -!- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES) AND IRREVERSIBLY INACTIVATES THEM, MAY FORM PART OF A TISSUE-SPECIFIC ACUTE RESPONSE TO REMODELING STIMULI.  
 CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.  
 CC -!- SIMILARITY: BELONGS TO THE TIMP FAMILY.  
 DB EMBL: AF156031; AAF17356.1; --  
 DR HSSP: P16035; 1BR9.  
 DR InterPro: IPR001820; TIMP.  
 DR Pfam: PF00965; TIMP; 1.  
 DR SMART: SM00206; TIMP; 1.  
 KW Metalloproteinase inhibitor.  
 FT NON TER 1 1  
 FT DISULFID 2 109 BY SIMILARITY.  
 FT DISULFID 116 121 BY SIMILARITY.  
 FT DISULFID 129 150 BY SIMILARITY.  
 FT NON TER 152  
 SQ SEQUENCE 152 AA; 17736 MW; 4050E5F5FC5B85E7 CRC64;  
 Query Match 29.5%; Score 297.5; DB 6; Length 152;  
 Best Local Similarity 38.6%; Pred. No. 1e-24; Mismatches 56; Indels 11; Gaps 5;  
 Matches 61; Conservative 30;  
 QY 13 CNSDLVIRAKFVGTPEVNO---TTLVQRYEIKMTKMYGFGALGDAADIRFVYTPAMESV 69  
 DB 2 CNSDIYIRAKVQCKLVKSGPCTIV--YTIKQMYRGFTK---PHQYHTEASESI 56  
 QY 70 GGFHRSNRSEEFILAGKLQDGLHITTCSPVAPWNSLSLAQRGFTTYTVCCECTV 129  
 DB 57 CGL--KLEVNKYQYLLTGRVYDGKMTGLCNFEYRMDQLTSLQKGLNRYHLGC-NCKI 113  
 QY 130 FPCLSIPCKLQSGTHCLMTDQLQSGSEKFGQSHLACL 167  
 DB 114 KSCYVLPFCVTSKNECLWDMLSNFGYQSGHYACI 151  
 RESULT 6  
 Q9TTB6 PRELIMINARY; PRT; 170 AA.  
 ID Q9TTB6;  
 AC 09TTB6;  
 DT 01-MAY-2000 (Tremblrel. 13, Created)  
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 DE Metalloproteinase inhibitor 4 (TIMP-4) (Tissue inhibitor of metalloproteinase-4) (Fragment).  
 GN TIMP-4.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Wang J.F., Boykiw R.H., Reno C.R., Hart D.A., Olson M.E.;  
 RT "Cloning and sequencing of porcine TIMPs."  
 RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.  
 CC -!- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES) AND IRREVERSIBLY INACTIVATES THEM.  
 CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.  
 CC -!- SIMILARITY: BELONGS TO THE TIMP FAMILY.

DR EMBL: AF156032; AAF17357.1; --  
 DR HSSP: P16035; 2TMP.  
 DR InterPro: IPR001820; TIMP.  
 DR Pfam: PF00965; TIMP; 1.  
 DR SMART: SM00206; TIMP; 1.  
 KW Metalloproteinase inhibitor.  
 FT NON TER 1 1  
 FT DISULFID 107 154 BY SIMILARITY.  
 FT DISULFID 112 117 BY SIMILARITY.  
 FT DISULFID 125 146 BY SIMILARITY.  
 FT NON TER 170 170  
 SQ SEQUENCE 170 AA; 19831 MW; 29B6412F2D42817D CRC64;  
 Query Match 27.9%; Score 282; DB 6; Length 170;  
 Best Local Similarity 36.2%; Pred. No. 5.8e-23;  
 Matches 51; Conservative 30; Mismatches 54; Indels 6; Gaps 4;  
 QY 37 REIKMTKMYKGFQALGDAADIRFVYTPAMESVCGFHRSHNRSEEFILAGL-LDGLIH 95  
 DB 21 REIKQIKMKFGFEKI---SDIQYITPFDSSLCC-VKLETSQKQYLLTQGLSDGKVF 76  
 QY 96 ITTCSFVAPWNSLSLAQRGFTTYTVCCECTVFPCLSPCKLQSGTHCLMTDQLQSS 155  
 DB 77 IHLGVIEFWENLSFLQRESLNHYHLNC-GQITTCYVVPCTISAPNECLMTDWLLEOK 135  
 QY 156 EKQFSRHLCAPREPGLCTW 176  
 DB 136 LVGYQAGHYVCKAKHADGTCW 156  
 RESULT 7  
 Q9TTB8 PRELIMINARY; PRT; 138 AA.  
 ID Q9TTB8;  
 AC 09TTB8;  
 DT 01-MAY-2000 (Tremblrel. 13, Created)  
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
 DE Metalloproteinase inhibitor 2 (TIMP-2) (Tissue inhibitor of metalloproteinase-2) (Fragment).  
 GN TIMP-2.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Wang J.F., Boykiw R.H., Reno C.R., Hart D.A., Olson M.E.;  
 RT "Cloning and sequencing of porcine TIMPs."  
 RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.  
 CC -!- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES) AND IRREVERSIBLY INACTIVATES THEM.  
 CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.  
 CC -!- PTM: THE ACTIVITY OF TIMP-2 IS DEPENDENT ON THE PRESENCE OF DISULFIDE BONDS.  
 CC -!- SIMILARITY: BELONGS TO THE TIMP FAMILY.  
 DB EMBL: AF156030; AAF17355.1; --  
 DR HSSP: P16035; 1BR9.  
 DR InterPro: IPR001820; TIMP.  
 DR Pfam: PF00965; TIMP; 1.  
 DR SMART: SM00206; TIMP; 1.  
 KW Metalloproteinase inhibitor.  
 FT NON TER 1 1  
 FT DISULFID 117 122 BY SIMILARITY.  
 FT NON TER 138 138  
 SQ SEQUENCE 138 AA; 15596 MW; F43F13651F45C348 CRC64;  
 Query Match 24.4%; Score 246.5; DB 6; Length 138;  
 Best Local Similarity 39.7%; Pred. No. 3.6e-19;  
 Matches 56; Conservative 19; Mismatches 51; Indels 15; Gaps 6;  
 QY 17 LVIRAKFVGTPEVNO-TTLVQ-----RYEIKMTKMYGFGALGDAADIRFVYTPAMESV 69  
 DB 1 VVIRAKAVSEKEDSGNDIYGNPIRIQYIEIKQIMFK-----GPKDIEFTYTPASSAV 55



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AC Q61720;
DT 01-NOV-1996 (TRENBLREL. 01, Created)
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
DE Messenger RNA fragment for mouse interferon beta (Type 1) coding for
DE the c-terminal part (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82247191; PubMed=6179042;
RA Skup D., Windass J.D., Sor F.S., George H., Williams B.R.,
RA Fukuhara H., De Maeyer-Guignard J., De Maeyer E.;
RT "Molecular cloning of partial cDNA copies of two distinct mouse IFN-
RT beta mRNAs."
RL Nucleic Acids Res. 10:3069-3084(1982).
DR EMBL; V00755; CAA24132.1; -.
DR HSSP; P01033; IUBA.
DR InterPro: IPR001820; TIMP.
DR Pfam; PF00965; TIMP; 1.
DR NON_TER 1
FT SEQUENCE 38 AA; 4390 MW; 7837C934C664BC7F CRC64;
SQ
Query Match 14.8%; Score 149.5; DB 11; Length 36;
Best Local Similarity 75.0%; Pred. No. 3.5e-09;
Matches 27; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

Oy 144 HCLMTDQLQSGSEKGFQSHLACLPREPGLCTWQSL 179
Db 1 HCLMTDQVLVQSE-DYQSRHFACLPRLGLCTWRSL 35

RESULT 12
Q80U22 PRELIMINARY; PRT; 97 AA.
AC Q80U22;
DT 01-MAR-2002 (TRENBLREL. 20, Created)
DT 01-MAR-2002 (TRENBLREL. 20, Last sequence update)
DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
DE Tissue inhibitor of metalloproteinase 2 (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8335;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95105266; PubMed=7806596;
RA Lecoc K., Jung J.-C., Fini M., Edwards D.R.;
RT "Role of Matrix Metalloproteinase in Metamorphic Tadpole Tail
RT Resorption."
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY037944; AAL01592.1; -.
DR InterPro: IPR001820; TIMP.
DR Pfam; PF00965; TIMP; 1.
DR SMART; SMO0206; TIMP; 1.
DR PROSITE; PS00288; TIMP; UNKNOWN_1.
DR NON_TER 1
FT SEQUENCE 97 AA; 10646 MW; DDE1F6CD749E5803 CRC64;
SQ
Query Match 12.8%; Score 129.5; DB 13; Length 97;
Best Local Similarity 49.1%; Pred. No. 1.6e-06;
Matches 27; Conservative 8; Mismatches 13; Indels 7; Gaps 2;
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ID Q9QUW9 PRELIMINARY; PRT; 25 AA.
AC Q9QUW9;
DT 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
DE ENDOMERIOSIS protein-II (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=96094433; PubMed=8530636;
RA Sharpe-Times K.L., Penney L.L., Zimmer R.L., Wright J.A., Zhang Y.,
RA Surewicz K.;
RT "Partial purification and amino acid sequence analysis of
RT endometriosis protein-II (ENDO-II) reveals homology with tissue
RT inhibitor of metalloproteinases-1 (TIMP-1).";
RL J. Clin. Endocrinol. Metab. 80:3784-3787(1995).
DR HSSP; P01033; IUBA.
DR InterPro: IPR001820; TIMP.
DR Pfam; PF00965; TIMP; 1.
DR PROSITE; PS00288; TIMP; 1.
FT SEQUENCE 25 AA; 2698 MW; 35129B2B74C1FPAF CRC64;
SQ
Query Match 12.3%; Score 124; DB 11; Length 25;
Best Local Similarity 84.0%; Pred. No. 1.3e-06;
Matches 21; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 1 CTCVPHPTAFNCNSDLVIRAKFVG 25
Db 1 CSCAPHTPTAFNCNSDLVIRAKFVG 25

RESULT 14
Q9QV13 PRELIMINARY; PRT; 25 AA.
AC Q9QV13;
DT 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
DE Collagenase inhibitor MS-31 (Fragment).
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE.
RX MEDLINE=95105266; PubMed=7806596;
RA Rosenthal R.A., Moses M.A., Shintani Y., Megyesi J.F., Langer R.,
RA Folkman J.;
RT "Purification and characterization of two collagenase inhibitors from
RT mouse sarcoma 180 conditioned medium.";
RL J. Cell. Biochem. 56:97-105(1994).
DR HSSP; P01033; IUBA.
DR InterPro: IPR001820; TIMP.
DR Pfam; PF00965; TIMP; 1.
DR PROSITE; PS00288; TIMP; 1.
FT SEQUENCE 25 AA; 2678 MW; 923226E82C1901FD CRC64;
SQ
Query Match 12.3%; Score 124; DB 11; Length 25;
Best Local Similarity 84.0%; Pred. No. 1.3e-06;
Matches 21; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 2 TCVPHPTAFNCNSDLVIRAKFVG 26
Db 1 SCAPHTPTAFNCNSDLVIRAKFVG 25

RESULT 15
Q962H0 PRELIMINARY; PRT; 280 AA.
AC Q962H0;
DT 01-DEC-2001 (TRENBLREL. 19, Created)
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DT 01-DEC-2001 (TRENBLrel. 19; Last sequence update)  
DT 01-JUN-2002 (TRENBLrel. 21; Last annotation update)  
DE Tensilin.  
OS Cucumaria frondosa.  
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
OC Holothuroidea; Dendrochirotacea; Dendrochirotida; Cucumariidae;  
OC Cucumaria.  
OX NCBI\_TaxID=36326;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Tipper J.P., Trotter J.A.;  
RT "Cloning of tensilin cDNA: the stiffening factor in sea cucumber inner  
RT dermis."  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY033934; AAK61535.1; -  
DR InterPro; IPR001820; TIMP.  
DR Pfam; PF00965; TIMP; 1.  
SQ SEQUENCE 280 AA; 31528 MW; 00A6273DF52DA241 CRC64;  
  
Query Match 10.6%; Score 106.5; DB 5; Length 280;  
Best Local Similarity 20.8%; Pred. NO. 0.0019;  
Matches 44; Conservative 34; Mismatches 75; Indels 59; Gaps 12;  
  
QY 3 CVPHPQTAFGNSDIVIRAKFV-----GTPEVYNQTLYQRYEIKWTKMYKGFQALGD 54  
DB 25 CSVKHPQHHCDFATFVMKVITIIDVLDROGGDKLIN-----AEINRSWKKGPS 72  
  
QY 55 AADIRFVYTPAMESVCGYFHRSHNRSEBFLIAG---KLQDG---LLHITTCFVAPMNSL 108  
DB 73 SCDFOF-YAPS--SFCG---ATFDSGDTYVVVTGKETS DGRYWLH-GSCDYMIKWDDM 125  
  
QY 109 SLAQRGFTKTYTGCECTVPPCLS-----IPCKLQSGTHC-----LWTD 149  
DB 126 SDQKAGFGGKYKARCQIAESLTAASVKVEDIAANDYPLATTYWTPTGCVYNPLMTR 185  
  
QY 150 QLLQSEKG-----FQSRHLACLREPGLCTW 176  
DB 186 QFV--GRKGSSVVDCEVDYGLCKPNEADKCQW 215

Search completed: December 17, 2002, 15:08:09  
Job time : 35.6276 secs



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RESULT 2
US-09-452-817-1
; Sequence 1, Application US/09452817
; Patent No. 6342374
; GENERAL INFORMATION:
; APPLICANT: Carmichael, David F
; APPLICANT: Anderson, David C
; APPLICANT: Stricklin, George P
; APPLICANT: Weiglus, Howard G
; TITLE OF INVENTION: Human Collagenase Inhibitor, Recombinant Vector System
; TITLE OF INVENTION: For Using Same And Recombinant-DNA Method For
; TITLE OF INVENTION: Manufacture Of Same
; FILE REFERENCE: Serial No. 6342374 09/452,817
; CURRENT APPLICATION NUMBER: US/09/452,817
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 08/474,553
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/050,739
; PRIOR FILING DATE: 1993-04-21
; PRIOR APPLICATION NUMBER: 07/853,018
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: 07/517,475
; PRIOR FILING DATE: 1990-05-01
; PRIOR APPLICATION NUMBER: 07/320,923
; PRIOR FILING DATE: 1989-03-08
; PRIOR APPLICATION NUMBER: 06/784,319
; PRIOR FILING DATE: 1985-10-04
; PRIOR APPLICATION NUMBER: 06/699,181
; PRIOR FILING DATE: 1985-02-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID-NO 1
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-452-817-1
Query Match 100.0%; Score 579; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 7.3e-71;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCVPPHPQTAFCSNLDLVIRAKFVGTPPEVNTTLYQRYEIKMTKMYKGFQALGDAADIRF 60
|
Db 1 CTCVPPHPQTAFCSNLDLVIRAKFVGTPPEVNTTLYQRYEIKMTKMYKGFQALGDAADIRF 60
|
Qy 61 VYTPAMESVCGYFHRSHNRSEEFLLAGLQDGLLHITTCSFVAPWN 106
|
Db 61 VYTPAMESVCGYFHRSHNRSEEFLLAGLQDGLLHITTCSFVAPWN 106
|

RESULT 3
US-08-588-163-5
; Sequence 5, Application US/08588163
; Patent No. 5643752
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: A NOVEL TISSUE INHIBITOR OF
; TITLE OF INVENTION: METALLOPROTEINASES
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/111,070
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/588,163
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Luther, Barbara J.
; REGISTRATION NUMBER: 33,954
; REFERENCE/DOCKET NUMBER: PF-0053
; TELECOMMUNICATION INFORMATION:
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; APPLICATION NUMBER: US/08/588,163
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Luther, Barbara J.
; REGISTRATION NUMBER: 33,954
; REFERENCE/DOCKET NUMBER: PF-0053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-852-0195
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 207 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: METALLOPROTEINASES
; CLONE: TIMP-1
US-08-588-163-5
Query Match 100.0%; Score 579; DB 1; Length 207;
Best Local Similarity 100.0%; Pred. No. 8.7e-71;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCVPPHPQTAFCSNLDLVIRAKFVGTPPEVNTTLYQRYEIKMTKMYKGFQALGDAADIRF 60
|
Db 24 CTCVPPHPQTAFCSNLDLVIRAKFVGTPPEVNTTLYQRYEIKMTKMYKGFQALGDAADIRF 83
|
Qy 61 VYTPAMESVCGYFHRSHNRSEEFLLAGLQDGLLHITTCSFVAPWN 106
|
Db 84 VYTPAMESVCGYFHRSHNRSEEFLLAGLQDGLLHITTCSFVAPWN 129
|

RESULT 4
US-09-111-070-5
; Sequence 5, Application US/09111070
; Patent No. 5914392
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: A NOVEL TISSUE INHIBITOR OF
; TITLE OF INVENTION: METALLOPROTEINASES
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/111,070
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/588,163
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Luther, Barbara J.
; REGISTRATION NUMBER: 33,954
; REFERENCE/DOCKET NUMBER: PF-0053
; TELECOMMUNICATION INFORMATION:
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TELEPHONE: 415-855-0555  
TELEFAX: 415-852-0195  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 207 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY: METALLOPROTEINASES  
CLONE: TIMP-1  
US-09-111-070-5

Query Match 100.0%; Score 579; DB 2; Length 207;  
Best Local Similarity 100.0%; Pred. No. 8.7e-71;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CTCVPHPTAFCSNDLVIRAKFVGTPEVNOTTLVQRYEIKMTKMYKGFQALGDADIRF 60  
24 CTCVPHPTAFCSNDLVIRAKFVGTPEVNOTTLVQRYEIKMTKMYKGFQALGDADIRF 83  
61 VYTPMESVCGYFHRSHNRSEEFLLAGKLDGLHITTCFVAPWN 106  
84 VYTPMESVCGYFHRSHNRSEEFLLAGKLDGLHITTCFVAPWN 129

RESULT 5  
US-08-849-764C-5  
Sequence 5, Application US/08849764C  
Patent No. 6300310

GENERAL INFORMATION:

APPLICANT: GREENE, JOHN M

TITLE OF INVENTION: HUMAN TISSUE INHIBITOR OF

METALLOPROTEINASE-4

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: HUMAN GENOME SCIENCES, INC.

STREET: 9410 KEY WEST AVENUE

CITY: ROCKVILLE

STATE: MD

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/849,764C

FILING DATE: 19-Sep-1997

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: MICHELE M. WALES

REGISTRATION NUMBER: 43,975

REFERENCE/DOCKET NUMBER: PFI48US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 301-309-8504

TELEFAX: 301-309-8439

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 207 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-08-849-764C-5

Query Match 100.0%; Score 579; DB 4; Length 207;  
Best Local Similarity 100.0%; Pred. No. 8.7e-71;

Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CTCVPHPTAFCSNDLVIRAKFVGTPEVNOTTLVQRYEIKMTKMYKGFQALGDADIRF 60  
DB 24 CTCVPHPTAFCSNDLVIRAKFVGTPEVNOTTLVQRYEIKMTKMYKGFQALGDADIRF 83  
QY 61 VYTPMESVCGYFHRSHNRSEEFLLAGKLDGLHITTCFVAPWN 106  
DB 84 VYTPMESVCGYFHRSHNRSEEFLLAGKLDGLHITTCFVAPWN 129

RESULT 6  
US-09-262-087-5  
Sequence 5, Application US/09262087  
Patent No. 6391853

GENERAL INFORMATION:

APPLICANT: GREENE, JOHN M

TITLE OF INVENTION: HUMAN TISSUE INHIBITOR OF

METALLOPROTEINASE-4

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: HUMAN GENOME SCIENCES, INC.

STREET: 9410 KEY WEST AVE

CITY: ROCKVILLE

STATE: MD

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/262,087

FILING DATE: 04-MAR-1999

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/463,261

FILING DATE: 05-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/14498

FILING DATE: 13-FEB-1994

ATTORNEY/AGENT INFORMATION:

NAME: A. ANDERS BROOKES

REGISTRATION NUMBER: 36,373

REFERENCE/DOCKET NUMBER: PFI48PID1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 301-309-8504

TELEFAX: 301-309-8439

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 207 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-262-087-5

Query Match 100.0%; Score 579; DB 4; Length 207;  
Best Local Similarity 100.0%; Pred. No. 8.7e-71;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVPHPTAFCSNDLVIRAKFVGTPEVNOTTLVQRYEIKMTKMYKGFQALGDADIRF 60  
DB 24 CTCVPHPTAFCSNDLVIRAKFVGTPEVNOTTLVQRYEIKMTKMYKGFQALGDADIRF 83  
QY 61 VYTPMESVCGYFHRSHNRSEEFLLAGKLDGLHITTCFVAPWN 106  
DB 84 VYTPMESVCGYFHRSHNRSEEFLLAGKLDGLHITTCFVAPWN 129

RESULT 7

US-08-463-261B-11  
; Sequence 11, Application US/08463261B  
; Patent No. 6448042  
; GENERAL INFORMATION:  
; APPLICANT: John M. Greene and Craig A. Rosen  
; TITLE OF INVENTION: Human Tissue Inhibitor of Metalloproteinase-4  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
; STREET: 9410 KEY WEST AVENUE  
; CITY: ROCKVILLE  
; STATE: MARYLAND  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 INCH DISKETTE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WORD PERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/463,261B  
; FILING DATE: 05-JUN-1995  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/14498  
; FILING DATE: 13-DEC-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KENLEY K. HOOVER  
; REGISTRATION NUMBER: 40,302  
; REFERENCE/DOCKET NUMBER: PFI48P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 301-610-5790  
; TELEFAX: 301-610-8439  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 207 AMINO ACIDS  
; TYPE: AMINO ACID  
; STRANDEDNESS:  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE: PROTEIN  
US-08-463-261B-11  
Query Match 100.0%; Score 579; DB 4; Length 207;  
Best Local Similarity 100.0%; Pred. No. 8.7e-71;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CTCVPPHPQTAFCSNLDVIRAKFVGTPVNTTLQRYEIKMTKMYKGFQALGDAADIRF 60  
Db 24 CTCVPPHPQTAFCSNLDVIRAKFVGTPVNTTLQRYEIKMTKMYKGFQALGDAADIRF 83  
Qy 61 VYTPAMESVCGYFHRSHNRSEEFLLAGLQDGLLHITTCSFVAPWN 106  
Db 84 VYTPAMESVCGYFHRSHNRSEEFLLAGLQDGLLHITTCSFVAPWN 129  
RESULT 8  
US-08-588-163-3  
; Sequence 3, Application US/08588163  
; Patent No. 5643752  
; GENERAL INFORMATION:  
; APPLICANT: Hawkins, Phillip R.  
; APPLICANT: Murty, Lynn E.  
; TITLE OF INVENTION: A NOVEL TISSUE INHIBITOR OF  
; TITLE OF INVENTION: METALLOPROTEINASES  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: US  
; ZIP: 94304  
; COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/588,163  
FILING DATE: Herewith  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Luther, Barbara J.  
REGISTRATION NUMBER: 33,954  
REFERENCE/DOCKET NUMBER: PF-0053  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-852-0195  
TELEX:  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 220 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY: METALLOPROTEINASES  
CLONE: TIMP-2  
US-08-588-163-3  
Query Match 40.4%; Score 234; DB 1; Length 220;  
Best Local Similarity 44.7%; Pred. No. 9e-24;  
Matches 51; Conservative 15; Mismatches 34; Indels 14; Gaps 5;  
Qy 1 CTCVPPHPQTAFCSNLDVIRAKFVGTPVNTTLQY-----RYEIKMTKMYKGFQALG 53  
Db 27 CSCSPVHPQAFCSNLDVIRAKVSEKESGNDIYGNPIKRIQYIKIKMKF-----G 81  
Qy 54 DAADIRFVYTPAMESVCGYFHRSHNRSEEFLLAGLQ-DGLLHITTCSFVAPWN 106  
Db 82 PEKIDIEFIYTPSSAVCG-VSLDVGGKKEYLIAGKAGDGKMKHITLCDFIIVPWD 134  
RESULT 9  
US-09-111-070-3  
; Sequence 3, Application US/09111070  
; Patent No. 5914392  
; GENERAL INFORMATION:  
; APPLICANT: Hawkins, Phillip R.  
; APPLICANT: Murty, Lynn E.  
; TITLE OF INVENTION: A NOVEL TISSUE INHIBITOR OF  
; TITLE OF INVENTION: METALLOPROTEINASES  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: US  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA: US/09/111,070  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/588,163  
; FILING DATE:



ATTORNEY/AGENT INFORMATION:  
NAME: Luther, Barbara J.  
REGISTRATION NUMBER: 33,954  
REFERENCE/DOCKET NUMBER: PF-0053  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-852-0195  
TELEX:  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 220 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY: METALLOPROTEINASES  
CLONE: TIMP-2  
US-09-111-070-3  
Query Match 40.4%; Score 234; DB 2; Length 220;  
Best Local Similarity 44.7%; Pred. No. 9e-24; Mismatches 34; Indels 14; Gaps 5;  
Matches 51; Conservative 15;  
Qy 1 CTCVPHPQTAFCSNDLVIRAFVGTPEVNO-TTLYQ-----RVEIKMTKMYKGFQALG 53  
Db 27 CSCSPVHPQOAFCSNDLVIRAKAVSEKVDGNDIYGNPIKRIYEIKI-KMFK-----G 81  
Qy 54 DAADIRFVYTPAMESVCGYFHRSHNRSEFLIAGKLQ-DGLHITTCSEFVAPWN 106  
Db 82 PKDIEFIYTPASSAVCG-VSLDVGSKKEYLLIAGKAKGSGKXKHITLDFPIVMD 134

## RESULT 10

US-08-849-764C-3  
Sequence 3, Application US/08849764C  
Patent No. 6300310  
GENERAL INFORMATION:  
APPLICANT: GREENE, JOHN M  
ROSEN, CRAIG  
TITLE OF INVENTION: HUMAN TISSUE INHIBITOR OF  
METALLOPROTEINASE-4  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
STREET: 9410 KEY WEST AVENUE  
CITY: ROCKVILLE  
STATE: MD  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/849,764C  
FILING DATE: 19-Sep-1997  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MICHELE M. WALES  
REGISTRATION NUMBER: 43,975  
REFERENCE/DOCKET NUMBER: PF148US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-309-8504  
TELEFAX: 301-309-8439  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 218 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-08-849-764C-3

Query Match 39.0%; Score 226; DB 4; Length 218;  
Best Local Similarity 44.2%; Pred. No. 1.1e-22;

Matches 50; Conservative 16; Mismatches 33; Indels 14; Gaps 5;

Qy 1 CTCVPHPQTAFCSNDLVIRAFVGTPEVNO-TTLYQRYEIKMTKMYKGFQALGD 54  
Db 27 CSCSPVHPQOAFCSNDLVIRAKAVSEKVDGNDIYGNPIKRIYEIKI-KMFK-----GP 80  
Qy 55 AADIRFVYTPAMESVCGYFHRSHNRSEFLIAGKLQ-DGLHITTCSEFVAPWN 106  
Db 81 EKDIIEFIYTPASSAVCG-VSLDVGSKKEYLLIAGKAKGSGKXKHITLDFPIVMD 132

## RESULT 11

US-09-262-087-3  
Sequence 3, Application US/09262087  
Patent No. 6391853  
GENERAL INFORMATION:  
APPLICANT: GREENE, JOHN M  
ROSEN, CRAIG  
TITLE OF INVENTION: HUMAN TISSUE INHIBITOR OF  
METALLOPROTEINASE-4  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
STREET: 9410 KEY WEST AVE  
CITY: ROCKVILLE  
STATE: MD  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/262,087  
FILING DATE: 04-MAR-1999  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/463,261  
FILING DATE: 05-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/14498  
FILING DATE: 13-FEB-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: A. ANDERS BROOKES  
REGISTRATION NUMBER: 36,373  
REFERENCE/DOCKET NUMBER: PF148PID1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-309-8504  
TELEFAX: 301-309-8439  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 218 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-262-087-3  
Query Match 39.0%; Score 226; DB 4; Length 218;  
Best Local Similarity 44.2%; Pred. No. 1.1e-22;  
Matches 50; Conservative 16; Mismatches 33; Indels 14; Gaps 5;  
Qy 1 CTCVPHPQTAFCSNDLVIRAFVGTPEVNO-TTLYQRYEIKMTKMYKGFQALGD 54  
Db 27 CSCSPVHPQOAFCSNDLVIRAKAVSEKVDGNDIYGNPIKRIYEIKI-KMFK-----GP 80  
Qy 55 AADIRFVYTPAMESVCGYFHRSHNRSEFLIAGKLQ-DGLHITTCSEFVAPWN 106



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:      FILING DATE:
:      CLASSIFICATION:
:      PRIOR APPLICATION DATA:
:      APPLICATION NUMBER:    08/588,163
:      FILING DATE:
:      ATTORNEY/AGENT INFORMATION:
:      NAME:    Luther, Barbara J.
:      REGISTRATION NUMBER:    33,954
:      REFERENCE/DOCKET NUMBER:    PF-0053
:      TELECOMMUNICATION INFORMATION:
:      TELEPHONE:    415-855-0555
:      TELEFAX:    415-852-0195
:      TELEX:
:      INFORMATION FOR SEQ ID NO:    4:
:      SEQUENCE CHARACTERISTICS:
:      LENGTH:    211 amino acids
:      TYPE:    amino acid
:      STRANDEDNESS:    single
:      TOPOLOGY:    linear
:      MOLECULE TYPE:    peptide
:      IMMEDIATE SOURCE:
:      LIBRARY:    METALLOPROTEINASES
:      CLONE:    TIMP-3
:      US-09-111-070-4

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Query Match	37.1%	Score 215, DB 2;	length 211;
Best Local Similarity	41.3%	Pred. No. 3.3e-21;	
Matches 45; Conservative	20;	Mismatches 34;	Indels 10; Gaps 4;

Qy 1 CTCVPHPCPAFNSLSLVIRAFVGTPEVNO--TTLYQRFKIEIMTCTMYGFOALDDAD 57  
Db 24 CTCSPHPQAFNSDVIIRAKVGVKKLVKGGPFTLV--TTIQMOMMYGFGFR---PH 78  
Qy 58 IRVVYPRMNSVCGYFHRSHNSSEFLAGLQGLAHITTCSEVAAWN 106  
Db 79 VQYIHHBASESLGL--KLEVNKYLQILLGRVYDKMKTGLCNVVERMD 125

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RESULT 15
US-08-849-764C-4
: Sequence 4, Application US/08849764C
: Patent No. 6300310
: GENERAL INFORMATION:
: APPLICANT: GREENE, JOHN M
: ROSEN, CRAIG
: TITLE OF INVENTION: HUMAN TISSUE INHIBITOR OF
: METALLOPROTEINASE-4
: NUMBER OF SEQUENCES: 11
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: HUMAN GENOME SCIENCES, INC.
: STREET: 9410 KEY WEST AVENUE
: CITY: ROCKVILLE
: STATE: MD
: COUNTRY: USA
: ZIP: 20850
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent in Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/849,764C
: FILING DATE: 19-Sep-1997
: CLASSIFICATION: <Unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME: MICHELE M. WALES
: REGISTRATION NUMBER: 43,975
: REFERENCE/DOCKET NUMBER: PF148US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 301-309-8504
: TELEFAX: 301-309-8439
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:

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?          LENGTH: 210 amino acids
?          TYPE: amino acid
?          STRANDEDNESS: single
?          TOPOLOGY: linear
?          MOLECULE TYPE: protein
?          SEQUENCE DESCRIPTION: SEQ ID NO: 4:
?          GS-08-849-764C-4

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Query Match	36.2%	Score 209.5;	DB 4;	Length 210;
Best Local Similarity	41.3%	Pred. No. 1.8e-20;		
Matches 45;	Conservative 18;	Mismatches 35;	Indels 11;	Gaps 4

Qy 1 CTCVPHPPTACNSDLVIRAKVGTSPVNO---TTLVORKEIMTMYGFPALDDAD 57  
Db 24 CTCSPHQDARCNMSDVIIRAKVCKKLKVGKRGPTLV--YTIIKQMYMGTFKPMYH-- 79

Qy 58 IRVVYPRMSEVCGYFHSHNRSEEFLLAGLQDGLLHTTSCSVAPWYN 106  
Db 80 --YIHHSEASSLGL--KLEVNKYQYLLLTGTVGVGKMTGLCNVBERWD 124

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Job time : 9.4069 secs

Search completed: December 17, 2002, 15:06:34  
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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 17, 2002, 15:04:26 ; Search time 23.7586 Seconds  
(without alignments)  
594.503 Million cell updates/sec

Title: US-09-452-817-2

Perfect score: 579  
Sequence: 1 CTCVPHPHQTAFCNSDLVIR.....GKLQDGLHTTCSFVAPWN 106

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Number of hits satisfying chosen parameters: 908470

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Post-processing: Minimum March 0%  
Maximum March 100%  
Listing first 45 summaries

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23: /SIDSz/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	579	100.0	127	23	AAU99886
2	579	100.0	128	23	AAU99887
3	579	100.0	184	23	AAU99875
4	579	100.0	204	23	ABP42206
5	579	100.0	207	7	ABP60786
6	579	100.0	207	7	ABP60725
7	579	100.0	207	7	ABP60592
8	579	100.0	207	18	AAW60309
9	579	100.0	207	20	AAV08933
10	579	100.0	207	21	AAI19073

11	579	100.0	207	22	AAW93377
12	579	100.0	207	22	AAW93171
13	579	100.0	522	23	AAU99883
14	579	100.0	522	23	AAU99885
15	579	100.0	580	23	AAU99882
16	579	100.0	580	23	AAU99889
17	576	99.5	207	7	AAW60593
18	565	97.6	207	16	AAW65005
19	558	96.4	183	21	AAW44149
20	508	87.7	207	16	AAW65003
21	507	87.6	206	16	AAW65006
22	494	85.3	207	16	AAW65004
23	491	84.8	162	23	ABP42434
24	484	83.6	212	23	ABP42381
25	458	79.1	205	16	AAW65007
26	428.5	74.0	207	16	AAW65008
27	239.5	41.4	192	11	AAW06895
28	236.5	40.8	193	23	AAW60277
29	236	40.8	47	7	AAW60276
30	235	40.6	194	23	AAW60276
31	234	40.4	194	21	ABW08904
32	234	40.4	220	11	AAW07955
33	234	40.4	220	15	AAW62769
34	234	40.4	220	16	AAW65009
35	234	40.4	220	19	AAW48253
36	234	40.4	220	20	AAW08931
37	234	40.4	220	21	AAW19074
38	234	40.4	220	23	ABP41537
39	234	40.4	237	23	AAW60278
40	233	40.2	194	23	AAW60278
41	233	40.2	220	21	ABW57031
42	227	39.2	220	11	AAW60276
43	227	39.2	220	15	AAW48256
44	227	39.2	220	19	AAW48256
45	218	37.7	212	16	AAW65002

#### ALIGNMENTS

RESULT 1	AAU99886	AAU99886 standard; Protein; 127 AA.
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AC	AAU99886;	
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DT	07-OCT-2002 (first entry)	
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DE	Human TIMP 1-127 protein.	
XX		
KW	TIMP 1-127; Alzheimer's disease; tumour angiogenesis;	Human polypeptide,
KW	malaria; emphysema; asthma; chronic obstructive pulmonary disease;	Human secreted pro
KW	cystic fibrosis; otitis media; otitis externa; HIV; psoriasis; eczema;	Human TIMP fusion prote
KW	human immunodeficiency virus; atopic dermatitis; muscular dystrophy;	Human TIMP fusion prote
KW	herpes; ulceration; sepsis; rheumatoid arthritis; periodontal disease;	Sequence of a glibb
KW	tumour metastasis; osteoporosis; Paget's disease; scleroderma;	Human tissue inhib
KW	glomerulonephritis; hypertension.	Human cancer assoc
XX		
OS	Homo sapiens.	Cattle tissue inh
XX		
PN	WO200250287-A2.	Rabbit tissue inh
XX		
PD	27-JUN-2002.	Pig tissue inhibit
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PF	18-DEC-2001; 2001WO-US49256.	Human ovarian anti
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PR	18-DEC-2000; 2000US-256699P.	Human TIMP-1, Hom
XX		
PR	20-NOV-2001; 2001US-331966P.	Human TIMP-1 prote
XX		
PA	(ARRI-) ARRIYA PHARM INC.	Inhibitor of tissu
XX		
PI	Barr PJ, Gibson HL, Pemberton P;	
XX		



XX 18-DEC-2001; 2001WO-US49256.  
 PF 18-DEC-2000; 2000US-256699P.  
 PR 20-NOV-2001; 2001US-331966P.  
 XX (ARRI-) ARRIVA PHARM INC.  
 PA  
 PI Barr PJ, Gibson HL, Pemberton P;  
 XX WPI: 2002-500631/53.  
 DR N-PSDB; ABR88017.  
 XX  
 PT Novel fusion protein useful for inhibiting protease activity associated  
 PT inhibitor comprising alpha 1-antitrypsin and a second protease  
 PT inhibitor -  
 XX  
 P Disclosure; Page 37; 134pp; English.  
 CC This invention relates to a novel fusion protein comprising a first  
 CC protease inhibitor comprising an alpha1-antitrypsin or its functionally  
 CC active portion and a second protease inhibitor or its functionally  
 CC active protein. The fusion proteins of the invention may act as an  
 CC inhibitor of protease activity. The fusion protein of the invention  
 CC is useful for inhibiting protease activity associated with a disorder  
 CC such as emphysema, asthma, chronic obstructive pulmonary disease,  
 CC cystic fibrosis, otitis media, otitis externa or HIV infection, or  
 CC for treating an individual suffering from or at risk for a disease or  
 CC disorder involving unwanted protease activity. The proteins are useful  
 CC for treating dermatological diseases such as atopic dermatitis, eczema  
 CC and psoriasis, inflammatory responses to viral infection, and for  
 CC treating herpes infection, corneal or epidermal ulceration, chronic  
 CC non-healing wounds, sepsis, rheumatoid arthritis, periodontal disease,  
 CC tumour metastasis and tumour angiogenesis, gastric ulceration,  
 CC osteoporosis, Paget's disease, glomerulonephritis, scleroderma, malaria,  
 CC bacterial infection, Alzheimer's disease, hypertension and muscular  
 CC dystrophy. The present sequence represents the human tissue inhibitor  
 CC of metalloproteases used to create the fusion protein of the invention.  
 XX  
 S0 Sequence 184 AA;  
 Query Match 100.0%; Score 579; DB 23; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 9,2e-65;  
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 CTCVPPHPOTAFCSNDLVIRAKFVGTPEVNQTLTYQRYEIKMTKMYKGFQALGDAADIRF 60  
 1 CTCVPPHPOTAFCSNDLVIRAKFVGTPEVNQTLTYQRYEIKMTKMYKGFQALGDAADIRF 60  
 Oy 61 VTPPMESVCGYFHRSHNSEEFLLAGKLODGLHITTCSPFAPNN 106  
 61 VTPPMESVCGYFHRSHNSEEFLLAGKLODGLHITTCSPFAPNN 106  
 Db 61 VTPPMESVCGYFHRSHNSEEFLLAGKLODGLHITTCSPFAPNN 106  
 RESULT 4  
 ABP42206  
 ID ABP42206 standard; Protein; 204 AA.  
 AC ABP42206;  
 XX  
 DT 22-AUG-2002 (first entry)  
 XX  
 DE Human ovarian antigen HCOG079, SEQ ID NO:3338.  
 XX  
 XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;  
 KW Human cancer; breast cancer; tumour; reproductive system disorder;  
 KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;  
 KW PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;  
 KW inflammatory condition; immune disorder; blood disorder;  
 KW cardiovascular disorder; respiratory disorder; neurological disorder;  
 KW gastrointestinal disorder; urinary system disorder; drug screening;  
 KW gene therapy; chromosome mapping; forensic analysis;

KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;  
 KW antiinflammatory; gynaecological; reproductive.  
 XX  
 OS Homo sapiens.  
 XX WO20020677-A1.  
 XX  
 PD 03-JAN-2002.  
 XX  
 PF 07-JUN-2001; 2001WO-US18569.  
 XX  
 PR 07-JUN-2000; 2000US-209467P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PI Birse CE, Rosen CA;  
 XX WPI: 2002-147878/19.  
 DR N-PSDB; ABO55283.  
 XX  
 PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,  
 PT useful in the prevention, treatment and diagnosis of cancer (e.g.  
 PT ovarian cancer), immune disorders, cardiovascular disorders and  
 PT neurological diseases -  
 XX  
 PS Claim 11; SEQ ID No 3338; 2922pp; English.  
 CC The invention relates to 2175 novel human ovarian antigens (ABP41054-  
 CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also  
 CC encompasses polypeptides 90% identical and polynucleotides 95% identical  
 CC to the sequences of the invention. The invention additionally relates to  
 CC recombinant vectors and host cells comprising human ovarian antigen  
 CC polynucleotides, antibodies against human ovarian antigens, and the use  
 CC of ovarian polynucleotides and polypeptides in diagnosing,  
 CC treating, prognosing or preventing various ovary and/or breast-related  
 CC disorders. Such conditions include ovarian cancer and breast cancer, and  
 CC metastatic tumours of ovarian or breast origin, reproductive system  
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation,  
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhea), endocrine  
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic  
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and  
 CC vaginitis), immune disorders (e.g., congenital and acquired  
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),  
 CC blood-related disorders (e.g., anaemia), cardiovascular disorders,  
 CC respiratory disorders, neurological disorders, gastrointestinal disorders  
 CC and urinary system disorders. Ovarian antigen polypeptides and  
 CC polynucleotides may also be used in screening for compounds which  
 CC modulate ovarian antigen expression or activity. The polynucleotides may  
 CC further be used for gene therapy, chromosome mapping, in the  
 CC identification of individuals and in forensic analysis, and the  
 CC polypeptides may be used as food additives or to prepare antibodies  
 CC useful in disease diagnosis, drug targeting and phenotyping. The present  
 CC sequence represents a human ovarian antigen of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 S0 Sequence 204 AA;  
 Query Match 100.0%; Score 579; DB 23; Length 204;  
 Best Local Similarity 100.0%; Pred. No. 1e-64;  
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 CTCVPPHPOTAFCSNDLVIRAKFVGTPEVNQTLTYQRYEIKMTKMYKGFQALGDAADIRF 60  
 22 CTCVPPHPOTAFCSNDLVIRAKFVGTPEVNQTLTYQRYEIKMTKMYKGFQALGDAADIRF 81  
 Db 61 VTPPMESVCGYFHRSHNSEEFLLAGKLODGLHITTCSPFAPNN 106  
 82 VTPPMESVCGYFHRSHNSEEFLLAGKLODGLHITTCSPFAPNN 127  
 RESULT 5

AAP60786  
ID AAP60786 standard; Protein; 207 AA.

XX

AC AAP60786;

XX

DT 08-AUG-1991 (first entry)

XX

DE Sequence of tissue inhibitor of metalloproteinase (TIMP).

XX

KW Connective tissue; extracellular matrix.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Peptide 1..23

FT /label= signal

FT Protein 24..207

FT Modified-site 53..55

FT /label= potential N-glycosylation site

FT Modified-site 101..103

FT /label= as above

XX

PN GB2169295-A.

XX

PD 09-JUL-1986.

XX

PF 06-JAN-1986; 86GB-0000199.

XX

PR 01-NOV-1985; 85GB-0026951.

XX

PR 07-JAN-1985; 85GB-0000341.

XX

PR 06-JAN-1986; 86GB-0000199.

XX

PR 07-JAN-1985; 85GB-0500341.

XX

PR 05-OCT-1983; 83BE-0897924.

XX

PA (CELL-) CELLTech LTD.

XX

PI Harris TJR, Reynolds JJ, Docherty AJP, Murphy G;

XX

DR WPI; 1986-177873/28.

XX

DR N-PSDB; AAN60538.

XX

PT Prodn. of metallo-proteinase inhibitors - by recombinant DNA

FT techniques

XX

PS Disclosure; Fig 3; 16pp; English.

XX

CC A gene with residues 64-684 of AAN60538 is claimed. AAN60538 was

CC isolated from human a foetal diploid lung cells (ATCC CLL153) cDNA

CC library using AAN60539.

XX

SQ Sequence 207 AA;

XX

Query Match 100.0%; Score 579; DB 7; Length 207;

Best Local Similarity 100.0%; Pred. No. 1.le-64;

Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCVPPHPQTAFCSNLDLVIKAFVGTPEVNTTLYQRYEIKMTKMYKGFQALGDAADIRF 60

Db 24 CTCVPPHPQTAFCSNLDLVIKAFVGTPEVNTTLYQRYEIKMTKMYKGFQALGDAADIRF 83

Qy 61 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCSFVAPWN 106

Db 84 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCSFVAPWN 129

RESULT 6

AAP60275

ID AAP60275 standard; Protein; 207 AA.

XX

AC AAP60275;

XX

DT 03-OCT-2002 (updated)

DT 08-AUG-1991 (first entry)

XX Sequence of human natural inhibitor of collagenases (NIC).

XX

KW Metallo-proteinase inhibitor; wound healing; emphysema;

XX rheumatoid arthritis therapy; ulceration; tumour metastasis.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Peptide 1..23

FT /label= signal

FT Protein 24..207

FT /note= "claimed"

FT Modified-site 53..55

FT /note= "potential glycosylation site"

FT Modified-site 101..103

FT /note= "potential glycosylation site"

XX

PN EPI89784-A.

XX

PD 06-AUG-1986.

XX

PF 16-JAN-1986; 86EP-0100482.

XX

PR 18-JAN-1985; 85US-0692808.

XX

PA (SEAR ) SEARLE G D & CO.

XX

XX Galloway WA, Clissold PM, McCullagh KG;

XX

DR WPI; 1986-205910/32.

XX

DR N-PSDB; AAN60277.

XX

PT New human natural inhibitor of collagenase - for treating e.g.

PT rheumatoid arthritis or ulceration, and new DNA sequences coding

PT for it

XX

PS Disclosure; Fig 2; 51pp; English.

XX

CC The patentors claim the AA SQ of human NIC, DNA sequences coding for

CC NIC, and its RNA analogues and plasmids contg. this DNA. NIC

CC inhibits the activity of metallo-proteinases, esp. of collagenase,

CC proteoglycanase, gelatinase or a leucocyte, macrophage or tumour

CC cell metallo-proteinase.

CC (Updated on 03-OCT-2002 to add missing OS field.)

XX

SQ Sequence 207 AA;

XX

Query Match 100.0%; Score 579; DB 7; Length 207;

Best Local Similarity 100.0%; Pred. No. 1.le-64;

Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCVPPHPQTAFCSNLDLVIKAFVGTPEVNTTLYQRYEIKMTKMYKGFQALGDAADIRF 60

Db 24 CTCVPPHPQTAFCSNLDLVIKAFVGTPEVNTTLYQRYEIKMTKMYKGFQALGDAADIRF 83

Qy 61 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCSFVAPWN 106

Db 84 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCSFVAPWN 129

RESULT 7

AAP60592

ID AAP60592 standard; Protein; 207 AA.

XX

AC AAP60592;

XX

DT 13-AUG-1991 (first entry)

XX

DE Sequence of a human protein having erythroid potentiating

DE activity (EPA).

XX

XX Erythroid precursor growth; anaemia therapy.

KW



```
XX Homo sapiens.
OS
XX WO8602100-A.
XX
XX 10-APR-1986.
XX
XX 01-OCT-1985; 85WO-5001900.
XX
XX 01-OCT-1984; 84US-0656590.
XX
XX (SANO ) SANDOZ LTD.
XX (REGC ) REGENTS OF UNIV OF CALIFO.
XX
XX Brown E, Clark S, Golde DW, Casson JC, Hewick R, Westbrook CA;
XX WPI; 1986-106663/16.
XX N-PSDB; AAN60494.
XX
XX Vectors contg. gene for protein having erythroid potentiating
XX activity - used for producing protein to stimulate growth and
XX formation of erythroid cells
XX
XX Disclosure; Fig 4; 59pp; English.
XX
XX The inventors claim human and gibbon EPA proteins (AAP60592, AAP60593)
XX and cDNA that encodes EPA (AAN60494, AAN60495). The EPA protein has a
XX biological activity of at least about 1,000,000 units per mg of
XX protein and has an apparent molecular weight of about 28,000 daltons.
XX
XX Sequence 207 AA;
SQ
Query Match 100.0%; Score 579; DB 7; Length 207;
Best Local Similarity 100.0%; Pred. No. 1,1e-64;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CTCVPHPQTAFCSNDLVIRAKFVGTPEVNTTLYQRYEIKMTKMYKGFQALGDADIRF 60
DB 24 CTCVPHPQTAFCSNDLVIRAKFVGTPEVNTTLYQRYEIKMTKMYKGFQALGDADIRF 83
OY 61 VYTPMESVCGYFHRSHNRSEEFLLAGKLDGLHITTCSFVAPWN 106
DB 84 VYTPMESVCGYFHRSHNRSEEFLLAGKLDGLHITTCSFVAPWN 129
XX
RESULT 8
AAN30309
AAN30309 standard; Protein; 207 AA.
XX
XX AAN30309;
XX
XX 29-JAN-1998 (first entry)
XX
XX Human TIMP-1.
XX
XX TIMP-3; human; antibody; TIMP-3-mediated disease; malignant tumour cell;
XX cancer progression; TIMP-1.
XX
XX Homo sapiens.
XX
XX JP09235300-A.
XX
XX 09-SEP-1997.
XX
XX 29-FEB-1996; 96JP-0067484.
XX
XX 29-FEB-1996; 96JP-0067484.
XX
XX 29-FEB-1996; 96JP-0067484.
XX
XX (FUJY ) FUJI PHARM IND CO LTD.
XX
XX WPI; 1997-498341/46.
XX
XX N-PSDB; AAT92631.
XX
```

```
PT Human TIMP-3 and anti-human TIMP-3 monoclonal antibodies - used in
PT diagnosis of TIMP-3 mediated diseases, especially the detection of
PT malignant tumour cells
XX
XX Example 12; Page 33-34; 37pp; Japanese.
XX
XX This sequence represents the human TIMP-1 protein. This sequence was
XX used to test the specificity of the monoclonal antibody (Mab) of the
XX invention. The Mab of the invention reacts specifically with human
XX TIMP-3 (see AAN30308), by specific recognition of the TIMP-3 fragments
XX represented by AAN30305-W30307. The Mab can be used in the study or
XX diagnosis of TIMP-3-mediated diseases, particularly for the detection of
XX malignant tumour cells, or the diagnosis of progressiveness of cancers.
XX They can also be used in establishing an immunoassay for TIMP-3 or in
XX purification of TIMP-3. The transformed cells can be used for producing
XX TIMP-3 or its equivalent proteins on a large scale. The immunoassay
XX method for TIMP-3 the Mabs is simple, highly reproducible and highly
XX sensitive.
XX
XX Sequence 207 AA;
SQ
Query Match 100.0%; Score 579; DB 18; Length 207;
Best Local Similarity 100.0%; Pred. No. 1,1e-64;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CTCVPHPQTAFCSNDLVIRAKFVGTPEVNTTLYQRYEIKMTKMYKGFQALGDADIRF 60
DB 24 CTCVPHPQTAFCSNDLVIRAKFVGTPEVNTTLYQRYEIKMTKMYKGFQALGDADIRF 83
OY 61 VYTPMESVCGYFHRSHNRSEEFLLAGKLDGLHITTCSFVAPWN 106
DB 84 VYTPMESVCGYFHRSHNRSEEFLLAGKLDGLHITTCSFVAPWN 129
XX
RESULT 9
AAY08933
AAY08933 standard; Protein; 207 AA.
XX
XX AAY08933;
XX
XX 19-AUG-1999 (first entry)
XX
XX Human TIMP-1 protein.
XX
XX TIMP-4; tissue inhibitor of metalloprotease; human; antibody; diagnosis;
XX treatment; metastasis; neoplastic cell; angiogenesis; tumour; cervical;
XX uterine; pancreatic; colon; intestinal carcinoma; pregnancy; ulcer;
XX osteoarthritis; pulmonary emphysema; periodontal disease; corneal;
XX rheumatoid arthritis; diabetic ulcer; lesion; TIMP-4.
XX
XX Homo sapiens.
XX
XX US5914392-A.
XX
XX 22-JUN-1999.
XX
XX 07-JUL-1998; 98US-0111070.
XX
XX 18-JAN-1996; 96US-0568163.
XX
XX 27-JUN-1997; 97US-0884073.
XX
XX 07-JUL-1998; 98US-0111070.
XX
XX (INCY-) INCYTE PHARM INC.
XX
XX Hawkins PR, Murry LE;
XX
XX WPI; 1999-384187/32.
XX
XX Anti-tissue inhibitor metalloproteinase antibodies useful for
XX treating and diagnosing cancer
XX
XX Disclosure; Fig 4; 26pp; English.
XX
```

CC This invention describes a novel method for the production of antibodies  
CC specific for the human tissue inhibitors of metalloproteinase 4, TIMP-4.  
CC The anti-TIMP-4 antibodies may be used to treat, prevent or diagnose  
CC metastasis of neoplastic cells, angiogenesis and growth tumours such as  
CC cervical, uterine, pancreatic, colon or intestinal carcinomas, pregnancy,  
CC osteoarthritis, pulmonary emphysema, peridontal disease, rheumatoid  
CC arthritis, corneal or diabetic ulcers or ulcers and lesions caused by  
CC microorganisms. This sequence represents TIMP-4 which is used to  
CC describe the method of the invention.

XX SQ Sequence 207 AA;  
Query Match 100.0%; Score 579; DB 20; Length 207;  
Best Local Similarity 100.0%; Pred. No. 1.1e-64;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CTCVPPHPQTAFCSNLDLVIRAKFVGTPEVNTTLVQRYEIKTKMYKGFQALGDAADIRF 60  
Db 24 CTCVPPHPQTAFCSNLDLVIRAKFVGTPEVNTTLVQRYEIKTKMYKGFQALGDAADIRF 83  
Qy 61 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCSFVAPWN 106  
Db 84 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCSFVAPWN 129

RESULT 10  
AAB19073  
ID AAB19073 standard; protein; 207 AA.  
XX AC AAB19073;  
XX DT 08-FEB-2001 (first entry)  
XX DE Inhibitor of tissue metalloproteinase designated TIMP-1.  
XX KW Tissue metalloproteinase inhibitor; TIMP; metalloproteinase; gelatinase;  
XX KW metastasis; cancer.  
XX OS Unidentified.

XX FH Key Location/Qualifiers  
XX FT Peptide 1..23  
XX FT /note= "signal peptide"  
XX FT Protein 24..207  
XX FT /note= "mature protein"  
XX PN EP1041083-A1.  
XX PD 04-OCT-2000.  
XX PF 03-APR-2000; 2000EP-0107041.  
XX PR 01-APR-1999; 99JP-0095142.  
XX PA (ORIY ) ORIENTAL YEAST CO LTD.  
XX PI Miyazaki K, Higashi S;  
XX WPI; 2000-603818/58.

XX PT New modified tissue inhibitor of metalloproteinases, useful for  
XX manufacturing compositions for inhibiting metastasis of cancer and  
XX PT vascularisation and for preventing or treating diseases associated with  
XX PT these, e.g. brain tumor  
XX PS Disclosure; Page 12-13; 25pp; English.  
XX CC The present sequence represents an inhibitor of tissue metalloproteinase,  
XX designated TIMP. The specification describes modified forms of TIMP,  
XX CC where the amino-terminal alpha-amino group is modified with an electron  
XX CC accepting group to substantially lose the ability to bind to a  
XX CC metalloproteinase. Modified TIMP-2 prevents an accumulation of active  
XX CC gelatinase. A on the cell surface, and can inhibit the activation of

CC precursor matrix metalloproteinases. The modified TIMP-2 and the  
CC compositions comprising TIMP-2 are useful for inhibiting metastasis of  
CC cancer and vascularisation. It is also used for treating diseases  
CC associated with them. Specifically, these are useful for preventing or  
CC treating metastasis of cancer of the stomach, colon, lung, head and  
CC neck, brain tumour, breast, thyroid, prostate, ovary or pancreas, or  
CC vascularisation or other conditions associated with these.

XX SQ Sequence 207 AA;  
Query Match 100.0%; Score 579; DB 21; Length 207;  
Best Local Similarity 100.0%; Pred. No. 1.1e-64;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CTCVPPHPQTAFCSNLDLVIRAKFVGTPEVNTTLVQRYEIKTKMYKGFQALGDAADIRF 60  
Db 24 CTCVPPHPQTAFCSNLDLVIRAKFVGTPEVNTTLVQRYEIKTKMYKGFQALGDAADIRF 83  
Qy 61 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCSFVAPWN 106  
Db 84 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCSFVAPWN 129

RESULT 11  
AAM93377  
ID AAM93377 standard; Protein; 207 AA.  
XX AC AAM93377;  
XX DT 06-NOV-2001 (first entry)  
XX DE Human polypeptide, SEQ ID NO: 2953.  
XX KW Human; full length cDNA; cDNA synthesis; oligo-capping.  
XX OS Homo sapiens.  
XX PN EP1130094-A2.  
XX PD 05-SEP-2001.  
XX PF 07-JUL-2000; 2000EP-0114089.  
XX PR 08-JUL-1999; 99JP-0194486.  
XX PR 11-JAN-2000; 2000JP-0118774.  
XX PR 02-MAY-2000; 2000JP-0183765.  
XX PA (HELI-) HELIX RES INST.

XX PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;  
XX PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
XX WPI; 2001-524255/58.  
XX N-PSDB; RAK94297.  
XX PT 830 Primers useful for synthesizing full length cDNA clones and their  
XX use in genetic manipulation  
XX PS Claim 8; SEQ ID NO 2953; 1380pp + sequence listing; English.

XX CC The invention relates to primers for synthesising full length cDNA  
XX clones. 830 cDNA molecules encoding a human protein have been  
XX isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA  
XX molecules have been determined. Primers for synthesising the full length  
XX cDNA are useful for clarifying the function of the protein encoded by  
XX the cDNA. The full length clones were obtained by construction of full  
XX length enriched cDNA libraries that were synthesised by the oligo-capping  
XX method. The primers enable the production of the full length cDNA easily  
XX without any special methods. The present sequence is a polypeptide  
XX CC encoded by a full length human cDNA of the invention.  
XX Note: The sequence data for this patent did not form part of the printed  
XX specification, but was obtained in CD-ROM format directly from EPO.

SQ Sequence 207 AA;  
 Query Match 100.0%; Score 579; DB 22; Length 207;  
 Best Local Similarity 100.0%; Pred. No. 1,1e-64;  
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVPPHQTAFCSNDLVIRAKFVGTPEVNOTTLVQRYEIKMTKMYKGFQALGDAADIRF 60  
 |||  
 DB 24 CTCVPPHQTAFCSNDLVIRAKFVGTPEVNOTTLVQRYEIKMTKMYKGFQALGDAADIRF 83  
 |||

QY 61 VYTPMESVCGYFHRSHNRSEEFLLAGKLDGLHITTCSPFAPWN 106  
 |||  
 DB 84 VYTPMESVCGYFHRSHNRSEEFLLAGKLDGLHITTCSPFAPWN 129  
 |||

RESULT 12  
 AAG89171  
 ID AAG89171 standard; Protein, 207 AA.

AA89171;  
 DT 11-SEP-2001 (first entry)  
 XX  
 DE Human secreted protein, SEQ ID NO. 291.  
 XX  
 KW Human; secreted protein; gene therapy; vaccine; treatment; diagnosis;  
 KW GENSET.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO200142451-A2.  
 XX  
 PD 14-JUN-2001.  
 XX  
 PF 07-DEC-2000; 2000MO-1B01938.  
 XX  
 PR 08-DEC-1999; 99US-0169629.  
 PR 06-MAR-2000; 2000US-0187470.  
 XX  
 PA (GST ) GENSET.  
 PI Dumas Milne Edwards J, Bougueleret L, Jobert S;  
 XX  
 DR MPI: 2001-367870/38.  
 DR N-PSDB; AAH64774.  
 XX

Full length GENSET human nucleic acids encoding potentially secreted proteins, useful in gene therapy and vaccination against a variety of diseases, and for diagnosis of those diseases -

PS Claim 21; Page 825; 921pp; English.

XX The invention relates to full length GENSET human nucleic acids encoding  
 CC potentially secreted proteins. The nucleic acids and the polypeptides  
 CC they encode may be used in the prevention, treatment and diagnosis of  
 CC diseases associated with inappropriate GENSET gene expression. For  
 CC example, they be used to treat disorders associated with decreased  
 CC GENSET gene expression by rectifying mutations or deletions in a  
 CC patient's genome that affect the activity of GENSET or by supplementing  
 CC the patient's own production of GENSET polypeptides. Conversely,  
 CC antisense nucleic acid molecules may be administered to down regulate  
 CC GENSET expression by binding with the cells' own genes and preventing  
 CC their expression. The sense and antisense nucleic acids may also be  
 CC used as DNA probes in diagnostic assays to detect and quantitate the  
 CC presence of similar nucleic acid sequences in samples, and hence to  
 CC determine which patients may be in need of restorative therapy.  
 CC The GENSET polypeptides may be used as antigens in the production of  
 CC antibodies and in assays to identify modulators (agonists and  
 CC antagonists) of GENSET polypeptide expression and activity. The  
 CC present sequence is a GENSET polypeptide of the invention.

XX Sequence 207 AA;

Query Match 100.0%; Score 579; DB 22; Length 207;  
 Best Local Similarity 100.0%; Pred. No. 1,1e-64;  
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVPPHQTAFCSNDLVIRAKFVGTPEVNOTTLVQRYEIKMTKMYKGFQALGDAADIRF 60  
 |||  
 DB 24 CTCVPPHQTAFCSNDLVIRAKFVGTPEVNOTTLVQRYEIKMTKMYKGFQALGDAADIRF 83  
 |||

QY 61 VYTPMESVCGYFHRSHNRSEEFLLAGKLDGLHITTCSPFAPWN 106  
 |||  
 DB 84 VYTPMESVCGYFHRSHNRSEEFLLAGKLDGLHITTCSPFAPWN 129  
 |||

RESULT 13  
 AAU99883  
 ID AAU99883 standard; Protein, 522 AA.

AAU99883;  
 AC  
 DT 07-OCT-2002 (first entry)  
 XX  
 DE NTAP1 fusion protein.  
 XX  
 KW NTAP1; Alzheimer's disease; tumour angiogenesis;  
 KW malaria; emphysema; asthma; chronic obstructive pulmonary disease;  
 KW cystic fibrosis; otitis media; otitis externa; HIV; psoriasis; eczema;  
 KW human immunodeficiency virus; atopic dermatitis; muscular dystrophy;  
 KW herpes; ulceration; sepsis; rheumatoid arthritis; periodontal disease;  
 KW tumour metastasis; osteoporosis; Paget's disease; scleroderma;  
 KW glomerulonephritis; hypertension.  
 XX  
 OS Homo sapiens.  
 OS  
 OS Synthetic.

Key Location/Qualifiers  
 FH 2..127  
 FT Region /note= "Human TIMP-1 amino acids 1-184"  
 FT 128  
 FT Region /note= "Linker methionine"  
 FT 129..522  
 FT Region /note= "Amino acids 1-394 of human AAT"

WO200250287-A2.  
 PD 27-JUN-2002.

PF 18-DEC-2001; 2001WO-US49256.  
 XX  
 PR 18-DEC-2000; 2000US-256699P.  
 PR 20-NOV-2001; 2001US-331966P.

PA (ARRI-) ARRIVA PHARM INC.

PI Barr PJ, Gibson HL, Pemberton P;

XX MPI: 2002-500631/53.  
 DR N-PSDB; ABK88024.

Novel fusion protein useful for inhibiting protease activity associated  
 with a disorder such as emphysema, asthma, comprises a first protease  
 inhibitor comprising alpha 1-antitrypsin and a second protease  
 inhibitor -

PS Example 2; Page 87; 134pp; English.

XX This invention relates to a novel fusion protein comprising a first  
 CC protease inhibitor comprising an alpha 1-antitrypsin or its functionally  
 CC active portion and a second protease inhibitor or its functionally  
 CC active protein. The fusion proteins of the invention may act as an  
 CC inhibitor of protease activity. The fusion protein of the invention  
 CC is useful for inhibiting protease activity associated with a disorder  
 CC such as emphysema, asthma, chronic obstructive pulmonary disease,  
 CC cystic fibrosis, otitis media, otitis externa or HIV infection, or

CC for treating an individual suffering from or at risk for a disease or  
 CC disorder involving unwanted protease activity. The proteins are useful  
 CC for treating dermatological diseases such as atopic dermatitis, eczema  
 CC and psoriasis, in inflammatory responses to viral infection, and for  
 CC treating herpes infection, corneal or epidermal ulceration, chronic  
 CC non-healing wounds, sepsis, rheumatoid arthritis, periodontal disease,  
 CC tumour metastasis and tumour angiogenesis, gastric ulceration,  
 CC osteoporosis, Paget's disease, glomerulonephritis, scleroderma, malaria,  
 CC bacterial infection, Alzheimer's disease, hypertension and muscular  
 CC dystrophy. The present sequence represents the NTAP1 fusion protein of  
 CC the invention.

XX SQ Sequence 522 AA;  
 Query Match 100.0%; Score 579; DB 23; Length 522;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-64;  
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CTCVPPHPQTAFCSNLDLVIKAFVGTPEVNTTLQRYEIKMTKMYKGFQALGDAADIRF 60  
 DB 2 CTCVPPHPQTAFCSNLDLVIKAFVGTPEVNTTLQRYEIKMTKMYKGFQALGDAADIRF 61  
 QY 61 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCSFVAPWN 106  
 DB 62 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCSFVAPWN 107

RESULT 14  
 AAU99885  
 ID AAU99885 standard; Protein; 522 AA.  
 XX  
 AC AAU99885;  
 DT 07-OCT-2002 (first entry)  
 XX  
 DE rN-TAP1 fusion protein.  
 XX  
 KW rN-TAP1; Alzheimer's disease; tumour angiogenesis;  
 KW malaria; emphysema; asthma; chronic obstructive pulmonary disease;  
 KW cystic fibrosis; otitis media; otitis externa; HIV; psoriasis; eczema;  
 KW human immunodeficiency virus; atopic dermatitis; muscular dystrophy;  
 KW herpes; ulceration; sepsis; rheumatoid arthritis; periodontal disease;  
 KW tumour metastasis; osteoporosis; Paget's disease; scleroderma;  
 KW glomerulonephritis; hypertension.

XX Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 2..395  
 FT /note= "Human AAT amino acids 1-394"  
 FT Region 396  
 FT /note= "Linker methionine"  
 FT Region 397..522  
 FT /note= "Amino acids 1-126 of human TIMP-1"  
 XX  
 PN WO200250287-A2.  
 XX  
 PD 27-JUN-2002.  
 XX  
 PF 18-DEC-2001; 2001WO-US49256.  
 XX  
 PR 18-DEC-2000; 2000US-256699P.  
 PR 20-NOV-2001; 2001US-331966P.  
 XX  
 PA (ARRI-) ARRIVA PHARM INC.  
 XX  
 PI Barr PJ, Gibson HL, Pemberton P;  
 PI WPI; 2002-500631/53.  
 DR N-PSDB; ABK88027.  
 XX  
 PT Novel fusion protein useful for inhibiting protease activity associated

PT with a disorder such as emphysema, asthma, comprises a first protease  
 PT inhibitor comprising alpha 1-antitrypsin and a second protease  
 XX inhibitor -

XX Example 3; Page 97; 134pp; English.

XX This invention relates to a novel fusion protein comprising a first  
 CC protease inhibitor comprising an alpha-antitrypsin or its functionally  
 CC active portion and a second protease inhibitor or its functionally  
 CC active protein. The fusion proteins of the invention may act as an  
 CC inhibitor of protease activity. The fusion protein of the invention  
 CC is useful for inhibiting protease activity associated with a disorder  
 CC such as emphysema, asthma, chronic obstructive pulmonary disease, or  
 CC cystic fibrosis, otitis media, otitis externa or HIV infection, or  
 CC for treating an individual suffering from or at risk for a disease or  
 CC disorder involving unwanted protease activity. The proteins are useful  
 CC for treating dermatological diseases such as atopic dermatitis, eczema  
 CC and psoriasis, in inflammatory responses to viral infection, and for  
 CC treating herpes infection, corneal or epidermal ulceration, chronic  
 CC non-healing wounds, sepsis, rheumatoid arthritis, periodontal disease,  
 CC tumour metastasis and tumour angiogenesis, gastric ulceration,  
 CC osteoporosis, Paget's disease, glomerulonephritis, scleroderma, malaria,  
 CC bacterial infection, Alzheimer's disease, hypertension and muscular  
 CC dystrophy. The present sequence represents the rN-TAP1 fusion protein of  
 CC the invention.

XX SQ Sequence 522 AA;  
 Query Match 100.0%; Score 579; DB 23; Length 522;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-64;  
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CTCVPPHPQTAFCSNLDLVIKAFVGTPEVNTTLQRYEIKMTKMYKGFQALGDAADIRF 60  
 DB 397 CTCVPPHPQTAFCSNLDLVIKAFVGTPEVNTTLQRYEIKMTKMYKGFQALGDAADIRF 456  
 QY 61 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCSFVAPWN 106  
 DB 457 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCSFVAPWN 502

RESULT 15  
 AAU99882  
 ID AAU99882 standard; Protein; 580 AA.  
 XX  
 AC AAU99882;  
 DT 07-OCT-2002 (first entry)  
 XX  
 DE TAP1 fusion protein.

XX  
 KW TAP1; Alzheimer's disease; tumour angiogenesis;  
 KW malaria; emphysema; asthma; chronic obstructive pulmonary disease;  
 KW cystic fibrosis; otitis media; otitis externa; HIV; psoriasis; eczema;  
 KW human immunodeficiency virus; atopic dermatitis; muscular dystrophy;  
 KW herpes; ulceration; sepsis; rheumatoid arthritis; periodontal disease;  
 KW tumour metastasis; osteoporosis; Paget's disease; scleroderma;  
 KW glomerulonephritis; hypertension.

XX Homo sapiens.  
 OS Synthetic.

XX  
 FH Key Location/Qualifiers  
 FT Region 2..185  
 FT /note= "Human TIMP-1 amino acids 1-184"  
 FT Region 186  
 FT /note= "Linker methionine"  
 FT Region 187..580  
 FT /note= "Amino acids 1-394 of human AAT"  
 XX  
 PN WO200250287-A2.  
 XX  
 PD 27-JUN-2002.

XX 18-DEC-2001; 2001WO-US49256.  
 PF  
 XX

PR 18-DEC-2000; 2000US-25669P.  
 PR 20-NOV-2001; 2001US-331966P.  
 XX

PA (ARRI-) ARRIVA PHARM INC.  
 XX

PI Barr PJ, Gibson HL, Pemberton P;  
 XX

DR MPI: 2002-500631/53.  
 DR N-PSDB; ABR88023.  
 XX

PT Novel fusion protein useful for inhibiting protease activity associated  
 with a disorder such as emphysema, asthma, comprises a first protease  
 PT inhibitor comprising alpha 1-antitrypsin and a second protease  
 PT inhibitor -  
 XX

XX Example 1; Page 79-82; 134pp; English.

CC This invention relates to a novel fusion protein comprising a first  
 CC protease inhibitor comprising an alpha1-antitrypsin or its functionally  
 CC active portion and a second protease inhibitor or its functionally  
 CC active protein. The fusion proteins of the invention may act as an  
 CC inhibitor of protease activity. The fusion protein of the invention  
 CC is useful for inhibiting protease activity associated with a disorder  
 CC such as emphysema, asthma, chronic obstructive pulmonary disease,  
 CC cystic fibrosis, otitis media, otitis externa or HIV infection, or  
 CC for treating an individual suffering from or at risk for a disease or  
 CC disorder involving unwanted protease activity. The proteins are useful  
 CC for treating dermatological diseases such as atopic dermatitis, eczema  
 CC and psoriasis, in inflammatory responses to viral infection, and for  
 CC treating herpes infection, corneal or epidermal ulceration, chronic  
 CC non-healing wounds, sepsis, rheumatoid arthritis, periodontal disease,  
 CC tumour metastasis and tumour angiogenesis, gastric ulceration,  
 CC osteoporosis, Paget's disease, glomerulonephritis, scleroderma, malaria,  
 CC bacterial infection, Alzheimer's disease, hypertension and muscular  
 CC dystrophy. The present sequence represents the TAPI fusion protein of  
 CC the invention.  
 CC  
 XX

XX Sequence 580 AA;

Query Match 100.0%; Score 579; DB 23; Length 580;  
 Best Local Similarity 100.0%; Pred. No. 4e-64;  
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTCVPPHPOTARCNSDLVIRAKVGTPEVNQTTLYRREIKMTKMYKGFQALGDADIRF 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 2 CTCVPPHPOTARCNSDLVIRAKVGTPEVNQTTLYRREIKMTKMYKGFQALGDADIRF 61

OY 61 VYTPMESVCGYFHRSHNRSEEFLLNGKLODGLLHTTCSFVAPWN 106  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 62 VYTPMESVCGYFHRSHNRSEEFLLNGKLODGLLHTTCSFVAPWN 107

Search completed: December 17, 2002, 15:06:04  
 Job time : 23.7586 secs

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: December 17, 2002, 15:04:31 ; Search time 10.6 Seconds  
(without alignments)  
961.344 Million cell updates/sec

Title: US-09-452-817-2

Perfect score: 579

Sequence: 1 CTCVPHPHQAFNCNSDLVIR.....GKLQDGLHITTCSEFVAPWN 106

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : PIR\_73:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	579	100.0	207	1	ZYHUP
2	579	100.0	207	2	UC4303
3	508	87.7	207	1	A35685
4	507	87.6	206	1	A33350
5	504	87.0	207	2	I46964
6	504	87.0	207	2	I47061
7	458	79.1	205	1	A26106
8	446	77.0	217	1	UC2557
9	234	40.4	220	1	A37128
10	233	40.2	196	1	S38624
11	233	40.2	220	1	JH0683
12	233	40.2	220	1	S45683
13	233	40.2	220	2	I53415
14	227	39.2	220	2	I53415
15	218	37.7	212	1	A43429
16	215	37.1	211	1	S45317
17	212	36.6	211	1	A53532
18	212	36.6	211	2	UC4630
19	74.5	12.9	50	2	I53729
20	74	12.8	158	2	R89123
21	72	12.4	530	2	N8MS
22	69	11.9	345	1	N8MS
23	67.5	11.7	421	2	T19315
24	66.5	11.5	490	2	F82973
25	66	11.4	464	2	E82517
26	66	11.4	572	2	UC5317
27	66	11.4	597	2	A82666
28	65	11.2	2549	2	A54837
29	64.5	11.1	195	2	AF1496

30	64.5	11.1	1005	2	T31333	beta-galactosidase
31	64	11.1	187	2	S25395	H+-transporting tw
32	64	11.1	932	2	UC5953	inter-alpha-inhibi
33	63.5	11.0	403	2	B71378	probable recf prot
34	63.5	11.0	1118	2	S57833	transmembrane prot
35	63	10.9	387	2	A86322	F6A14.9 protein -
36	63	10.9	1056	2	S58889	collapsin response
37	63	10.9	1056	2	T33167	hypothetical prote
38	63	10.9	1123	1	WMBEH7	u137 protein - hum
39	62	10.7	433	1	B65058	fixC protein homol
40	62	10.7	698	2	H71535	hypothetical prote
41	62	10.7	1426	2	T00337	hypothetical prote
42	62	10.7	1799	2	AD1895	serine/threonine k
43	61.5	10.6	250	2	G83276	precorrin-3 methyl
44	61.5	10.6	332	2	JC5465	2,3-dihydroxybiphe
45	61.5	10.6	562	2	A86773	hypothetical prote

#### ALIGNMENTS

RESULT 1  
ZYHUP  
metalloproteinase tissue inhibitor 1 precursor [validated] - human  
N:Alternate names: erythroid potentiating activity (EPA); fibroblast collagenase inhibitor  
C:Species: Homo sapiens (man)  
C:Date: 28-May-1986 #sequence revision 28-May-1986 #text change 08-Dec-2000  
A:Accession: A93372; A93363; A20555; A35826; A48417; S20318; S15872; I52912; S664  
R:Docterly, A.O.P.; Lyons, A.; Smith, B.U.; Wright, E.M.; Stephens, P.E.; Harris, T.D.R.;  
Nature 318, 66-69, 1985  
A>Title: Sequence of human tissue inhibitor of metalloproteinases and its identity to ery  
A:Reference number: A93372; MUID:86040463; PMID:3903517  
A:Accession: A93372  
A:Molecule type: mRNA  
A:Residues: 1-207 <DOC>  
A:Cross-references: GB:X03124; NID:G37182; PIDN:CAA26902.1; PID:G37183  
R:Gasson, J.C.; Golde, D.W.; Kaufman, S.E.; Westbrook, C.A.; Hewick, R.M.; Kaufman, R.J.;  
Nature 315, 768-771, 1985  
A>Title: Molecular characterization and expression of the gene encoding human erythroid-1  
A:Reference number: A93363; MUID:85240567; PMID:3838290  
A:Accession: A93363  
A:Molecule type: mRNA  
A:Residues: 1-207 <GAS>  
R:Camichael, D.F.; Sommer, A.; Thompson, R.C.; Anderson, D.C.; Smith, C.G.; Welgus, H.G.  
Proc. Natl. Acad. Sci. U.S.A. 83, 2407-2411, 1986  
A>Title: Primary structure and cDNA cloning of human fibroblast collagenase inhibitor.  
A:Reference number: A23534; MUID:86205964; PMID:3010309  
A:Accession: A23534  
A:Molecule type: mRNA  
A:Residues: 1-207 <CAR>  
A:Cross-references: GB:M2670; NID:G182482; PIDN:AAA52436.1; PID:G182483  
A>Note: parts of this sequence were confirmed by protein sequencing  
A>Note: carbohydrate binding sites were determined  
R:Stricklin, G.P.; Welgus, H.G.  
J. Biol. Chem. 258, 12252-12258, 1983  
A>Title: Human skin fibroblast collagenase inhibitor.  
A:Reference number: A20595; MUID:84032401; PMID:6313647  
A:Accession: A20595  
A:Molecule type: protein  
A:Residues: 24-44, 'L', 46 <STR>  
A>Note: six disulfide bonds are present  
R:Rapp, G.; Freudenstein, J.; Klaudiny, J.; Mucha, J.; Wempe, F.; Zimmer, M.; Scheit, K.  
DNA Cell Biol. 9, 479-485, 1990  
A>Title: Characterization of three abundant mRNAs from human ovarian granulosa cells.  
A:Reference number: A35826; MUID:91025550; PMID:2171551  
A:Accession: A35826  
A:Molecule type: mRNA  
A:Residues: 1-207 <RAP>  
A:Cross-references: GB:M8188  
R:Van Ransst, M.; Norga, K.; Masure, S.; Proost, P.; Vandekerckhove, F.; Auwerx, J.; Van I  
Cytokine 3, 231-239, 1991  
A>Title: The cytokine-protease connection: identification of a 96-kD THF-1 gelatinase and  
A:Reference number: A48417; MUID:91355647; PMID:1653055

A:Accession: A48417  
A:Molecule type: protein  
A:Residues: 'X', 25, 'X', 27-35, 'X', 37-52 <VAN>  
A:Experimental source: monocytic cell line THP-1  
A:Note: sequence modified after extraction from NCBI backbone  
A:Note: sequence incorrectly identified as 96K gelatinase  
R:Osrhues, A.; Knaeuper, V.; Oberhoff, R.; Reinke, H.; Tschesche, H.  
FEBS Lett. 296, 16-20, 1992  
A:Title: Isolation and characterization of tissue inhibitors of metalloproteinases (TIMP)  
A:Reference number: S20318; MUID:92111776; PMID:1730286  
A:Accession: S20318  
A:Molecule type: protein  
A:Residues: 'X', 25, 'X', 27-35, 'X', 37-38 <OST>  
A:Experimental source: rheumatoid synovial fluid  
R:Opdenakker, G.;ASURE, S.; Proost, P.; Billiau, A.; van Damme, J.  
FEBS Lett. 284, 73-78, 1991  
A:Title: Natural human monocyte Gelatinase and its inhibitor.  
A:Reference number: S15872; MUID:91285112; PMID:1647974  
A:Accession: S15872  
A:Molecule type: protein  
A:Residues: 'X', 25, 'X', 27-35, 'X', 37-42, 'X', 44, 'X', 46, 'X', 48-51 <FEB>  
A:Experimental source: peripheral blood monocytes  
R:Williamson, R.A.; Marston, F.A.O.; Angal, S.; Koklitis, P.; Panico, M.; Morris, H.R.;  
Biochem. J. 268, 267-274, 1990  
A:Title: Disulphide bond assignment in human tissue inhibitor of metalloproteinases (TIMP)  
A:Reference number: A38978; MUID:90303199; PMID:2163605  
A:Contents: annotation; disulfide bonds  
R:Opbroek, A.; Kenney, M.C.; Brown, D.  
Curt. Eye Res. 12, 877-883, 1993  
A:Title: Characterization of a human corneal metalloproteinase inhibitor (TIMP-1).  
A:Reference number: 152912; MUID:94123576; PMID:7507419  
A:Accession: 152912  
A:Status: translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-207 <RES>  
A:Cross-references: GB:S68252; NID:G545022; PIDN:AAD14009.1; PID:G4261709  
R:Triebel, S.; Blaaser, J.; Gore, T.; Pelz, G.; Schueren, E.; Schmitt, M.; Tschesche, H.  
Eur. J. Biochem. 231, 714-719, 1995  
A:Title: Evidence for the tissue inhibitor of metalloproteinases-1 (TIMP-1) in human pol  
A:Reference number: S66461; MUID:95377303; PMID:7649172  
A:Accession: S66461  
A:Molecule type: protein  
A:Residues: 24-38 <TRI>  
A:Experimental source: polymorphonuclear leukocytes  
C:Comment: This protein, found in a variety of body fluids, complexes with metalloprotei  
s-specific, stimulating the growth and differentiation of only human and murine erythro  
C:Comment: The remarkable heat stability of this protein may be due to disulfide bond fo  
C:Genetics:  
A:Gene: GDB:TIMP1; CLGI; TIMP  
A:Cross-references: GDB:I19615; OMTM:305370  
A:Map position: Xp11.3-Xp11.23  
C:Superfamily: metalloproteinase inhibitor  
C:Keywords: erythropoiesis; glycoprotein; metalloproteinase inhibitor  
F:1-23/Domain: signal sequence #status predicted <SIG>  
F:24-207/Product: metalloproteinase inhibitor 1 #status experimental <WAT>  
F:24-93,26-122,136-147,150-197,155-160,168-189/Disulfide bonds: #status experimental  
F:53,101/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 100.0%; Score 579; DB 1; Length 207;  
Best Local Similarity 100.0%; Pred. No. 5.3e-58;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCVPPHPQTAFCSNLDLVIKAFVGTPEVNQTTLYQRYEIKMTKMYKGFQALGDAADIRF 60  
Db 24 CTCVPPHPQTAFCSNLDLVIKAFVGTPEVNQTTLYQRYEIKMTKMYKGFQALGDAADIRF 83

Qy 61 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCSFVAPWN 106  
Db 84 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCSFVAPWN 129

RESULT 2  
JC4303

matrix metalloproteinase-1 tissue inhibitor - baboon  
C:Species: Papio sp. (baboon)  
C:Date: 16-Nov-1995 #sequence\_revision 08-Feb-1996 #text\_change 16-Jul-1999  
C:Accession: JC4303  
R:Forough, R.; Nikkari, S.T.; Hasenstab, D.; Lea, H.; Clowes, A.W.  
Gene 163, 267-271, 1995  
A:Title: Cloning and characterization of a cDNA encoding the baboon tissue inhibitor of  
A:Reference number: JC4303; MUID:96011646; PMID:7590279  
A:Accession: JC4303  
A:Molecule type: mRNA  
A:Residues: 1-207 <FOR>  
A:Cross-references: GB:L37295; NID:G561545; PIDN:AAA99943.1; PID:G561546  
A:Experimental source: smooth muscle cell  
C:Comment: This protein, a member of the tissue inhibitor of matrix metalloproteinase f  
se and influences the proteinase activity. It has a role as a physiological molecule f  
C:Genetics:  
A:Gene: timp-1  
C:Superfamily: metalloproteinase inhibitor  
C:Keywords: extracellular matrix; glycoprotein; metalloproteinase inhibitor  
F:53,101/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 579; DB 2; Length 207;  
Best Local Similarity 100.0%; Pred. No. 5.3e-58;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCVPPHPQTAFCSNLDLVIKAFVGTPEVNQTTLYQRYEIKMTKMYKGFQALGDAADIRF 60  
Db 24 CTCVPPHPQTAFCSNLDLVIKAFVGTPEVNQTTLYQRYEIKMTKMYKGFQALGDAADIRF 83

Qy 61 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCSFVAPWN 106  
Db 84 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCSFVAPWN 129

RESULT 3  
A35685  
Metalloproteinase inhibitor 1 precursor - bovine  
N:Alternate names: cartilage-derived neovascularization inhibitor; TIMP-1; tissue inhib  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 21-Sep-1990 #sequence\_revision 12-Apr-1996 #text\_change 18-Jun-1999  
C:Accession: A35685; B34468; B29712; A34833; I46979  
R:Freudenstein, J.; Wagner, S.; Luck, R.M.; Einspanier, R.; Scheit, K.H.  
Biochem. Biophys. Res. Commun. 171, 250-256, 1990  
A:Title: mRNA of bovine tissue inhibitor of metalloproteinase: sequence and expression  
A:Reference number: A35685; MUID:90365711; PMID:2393392  
A:Accession: A35685  
A:Molecule type: mRNA  
A:Residues: 1-207 <PRE>  
A:Cross-references: GB:M60073; NID:G163760; PIDN:AAA30784.1; PID:G163761  
A:Experimental source: ovary cDNA library  
R:De Clerck, Y.A.; Yean, T.D.; Ratzkin, B.J.; Lu, H.S.; Langley, K.E.  
J. Biol. Chem. 264, 17445-17453, 1989  
A:Title: Purification and characterization of two related but distinct metalloproteinase  
A:Reference number: A34468; MUID:90008914; PMID:2551903  
A:Accession: B34468  
A:Molecule type: protein  
A:Residues: 24-52, 'X', 54-57, 'LY', 60-61, 'L', 63-65, 'L', 67-68, 'P', <DEC>  
A:Experimental source: culture medium of aortic endothelial cells  
R:Kaczorek, M.; Honore, N.; Ribes, V.; Dehoux, P.; Cornet, P.; Cartwright, T.; Streech,  
Bio/Technology 5, 595-598, 1987  
A:Title: Molecular cloning and synthesis of biologically active human tissue inhibitor  
A:Reference number: A29712  
A:Accession: B29712  
A:Molecule type: protein  
A:Residues: 24-37 <KAC>  
A:Experimental source: culture medium of fibroblastic BC 21 cells  
A:Note: protein inhibits angiogenesis  
R:Moses, M.A.; Sudhalter, J.; Langer, R.  
Science 248, 1408-1410, 1990  
A:Title: Identification of an inhibitor of neovascularization from cartilage.  
A:Reference number: A34833; MUID:90288433; PMID:1694043  
A:Accession: A34833  
A:Molecule type: protein



A,Residues: 24-51 <MOS>  
 A,Experimental source: cartilage  
 R:Satoch, T.; Kobayashi, K.; Yamashita, S.; Kikuchi, M.; Sendai, Y.; Hoshi, H.  
 Biol. Reprod. 50: 835-844, 1994  
 A,Title: Tissue inhibitor of metalloproteinases (TIMP-1) produced by granulosa and oviduct  
 A,Reference number: 146979; MUID:94257757; PMID:8199264  
 A,Accession: 146979  
 A,Status: translated from GB/EMBL/DBJ  
 A,Molecule type: mRNA  
 A,Residues: 1-207 <SAT>  
 A,Cross-references: GB:S70841; NID:9546973; PIDN:AA30892.1; PID:9546974  
 C,Function:  
 A,Description: regulation of extracellular matrix remodeling by inhibition of matrix met  
 possibly controlling their activation. TIMP-1 and TIMP-2 possess erythroid potentiating  
 A>Note: transcription induced by cytokines, tumor promoters, and anti-inflammatory agent  
 A>Note: TIMP-1 and TIMP-3 have distinct but overlapping tissue-specific expression patte  
 C,Superfamily: metalloproteinase inhibitor  
 C,Keywords: erythropoiesis; extracellular matrix; glycoprotein; metalloproteinase inhibi  
 F:1-207/Product: metalloproteinase inhibitor 1 #status experimental <MAT>  
 F:1-93,26-122,36-147,150-197,155-160,168-189/Disulfide bonds: #status predicted  
 F:53,101/Binding site: carbonyl (Asn) (covalent) #status predicted

Query Match 87.7%; Score 508; DB 1; Length 207;  
 Best Local Similarity 86.8%; Pred. No. 5,9e-50;  
 Matches 92; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Oy 1 CTCVPHPHQTACNSDVLVIRAFVGTPEVNOITLYORIEIKTKTKYKGGQALGDAADIRF 60  
 Db 24 CTCVPHPHQTACNSDVLVIRAFVGTAEVNETALYORIEIKTKTKMGKFSALRDADIRF 83  
 Oy 61 VYTPMESVCGYFHRSHNRSEEFLLAGKLDGDLHITTCSPFAPWN 106  
 Db 84 IYTPMESVCGYFHRSHNRSEEFLLAGQLSNGHLHITTCSPFAPWN 129

## RESULT 4

A33350  
 metalloproteinase inhibitor 1 precursor - rabbit  
 N,Alternate names: TIMP-1; tissue inhibitor of metalloproteinases 1  
 C,Species: Oryctolagus cuniculus (domestic rabbit)  
 C,Date: 30-Jun-1992 #sequence\_revision 12-Apr-1996 #text\_change 18-Jun-1999  
 C,Accession: A33350; A30864  
 R:Horowitz, S.; Dafni, N.; Shapiro, D.L.; Holm, B.A.; Notter, R.H.; Quidle, D.J.  
 J. Biol. Chem. 264: 7092-7095, 1989  
 A,Title: Hyperoxic exposure alters gene expression in the lung. Induction of the tissue  
 A,Reference number: A33350; MUID:89214135; PMID:2708356  
 A,Accession: A33350  
 A,Molecule type: mRNA  
 A,Residues: 1-206 <HOR>  
 A,Cross-references: GB:J04712; NID:9165742; PIDN:AAA31478.1; PID:9165743  
 A,Experimental source: hyperoxia-exposed lung of New Zealand white rabbits  
 C,Comment: Expression of this protein in the lung is induced 6-fold by hyperoxia.  
 C,Function:  
 A,Description: regulation of extracellular matrix remodeling by inhibition of matrix met  
 possibly controlling their activation. TIMP-1 and TIMP-2 possess erythroid potentiating  
 A>Note: transcription induced by cytokines, tumor promoters, and anti-inflammatory agent  
 A>Note: TIMP-1 and TIMP-3 have distinct but overlapping tissue-specific expression patte  
 C,Superfamily: metalloproteinase inhibitor  
 C,Keywords: erythropoiesis; extracellular matrix; glycoprotein; metalloproteinase inhibi  
 F:1-23/Domain: signal sequence #status predicted <SIG>  
 F:1-24-206/Product: metalloproteinase inhibitor 1 #status predicted <MAT>  
 F:24-93,26-122,36-147,150-196,155-160,168-188/Disulfide bonds: #status predicted  
 F:53,101/Binding site: carbonyl (Asn) (covalent) #status predicted

Query Match 87.6%; Score 507; DB 1; Length 206;  
 Best Local Similarity 86.8%; Pred. No. 7,6e-50;  
 Matches 92; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Oy 1 CTCVPHPHQTACNSDVLVIRAFVGTPEVNOITLYORIEIKTKTKYKGGQALGDAADIRF 60  
 Db 24 CTCVPHPHQTACNSDVLVIRAFVGTAEVNETALYORIEIKTKTKMGKFSALRDADIRF 83

Oy 61 VYTPMESVCGYFHRSHNRSEEFLLAGKLDGDLHITTCSPFAPWN 106  
 Db 84 VYTPMESVCGYFHRSHNRSEEFLLAGQLSNGHLHITTCSPFAPWN 129

## RESULT 5

A14964  
 metalloproteinase tissue inhibitor 1 precursor [similarity] - sheep  
 C,Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
 C,Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 19-Jan-2001  
 C,Accession: 146964  
 R:Smith, G.W.; Goetz, T.L.; Anthony, R.V.; Smith, M.F.  
 Endocrinology 134, 344-352, 1994  
 A,Title: Molecular cloning of an ovine ovarian tissue inhibitor of metalloproteinases: or  
 eal tissue.  
 A,Reference number: 146964; MUID:94102210; PMID:8275949  
 A,Accession: 146964  
 A,Status: preliminary; translated from GB/EMBL/DBJ  
 A,Molecule type: mRNA  
 A,Residues: 1-207 <SMI>  
 A,Cross-references: GB:S67450; NID:9456989; PIDN:AA829472.1; PID:9456990  
 C,Superfamily: metalloproteinase inhibitor

Query Match 87.0%; Score 504; DB 2; Length 207;  
 Best Local Similarity 85.8%; Pred. No. 1,7e-49;  
 Matches 91; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Oy 1 CTCVPHPHQTACNSDVLVIRAFVGTPEVNOITLYORIEIKTKTKYKGGQALGDAADIRF 60  
 Db 24 CTCVPHPHQTACNSDVLVIRAFVGTAEVNETALYORIEIKTKTKMGKFSALRDADIRF 83  
 Oy 61 VYTPMESVCGYFHRSHNRSEEFLLAGKLDGDLHITTCSPFAPWN 106  
 Db 84 IYTPMESVCGYFHRSHNRSEEFLLAGQLSNGHLHITTCSPFAPWN 129

## RESULT 6

A147061  
 collagenase inhibitor - pig  
 C,Species: Sus scrofa domestica (domestic pig)  
 C,Date: 04-Sep-1997 #sequence\_revision 04-Sep-1997 #text\_change 16-Jul-1999  
 C,Accession: 147061  
 R:Tanaka, T.; Andoh, N.; Takeya, T.; Sato, E.  
 Mol. Cell. Endocrinol. 83, 65-71, 1992  
 A,Title: Differential screening of ovarian cDNA libraries detected the expression of the  
 A,Reference number: 147061; MUID:92201478; PMID:1312961  
 A,Accession: 147061  
 A,Status: preliminary; translated from GB/EMBL/DBJ  
 A,Molecule type: mRNA  
 A,Residues: 1-207 <TAN>  
 A,Cross-references: GB:S86211; NID:9247729; PIDN:AA821865.1; PID:9247730  
 C,Superfamily: metalloproteinase inhibitor

Query Match 87.0%; Score 504; DB 2; Length 207;  
 Best Local Similarity 85.8%; Pred. No. 1,7e-49;  
 Matches 91; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

Oy 1 CTCVPHPHQTACNSDVLVIRAFVGTPEVNOITLYORIEIKTKTKYKGGQALGDAADIRF 60  
 Db 24 CTCVPHPHQTACNSDVLVIRAFVGTAEVNETALYORIEIKTKTKMGKFSALRDADIRF 83  
 Oy 61 VYTPMESVCGYFHRSHNRSEEFLLAGKLDGDLHITTCSPFAPWN 106  
 Db 84 IYTPMESVCGYFHRSHNRSEEFLLAGQLSNGHLHITTCSPFAPWN 129

## RESULT 7

A26106  
 metalloproteinase inhibitor 1 precursor - mouse  
 N,Alternate names: erythroid potentiating activity (EPA); fibroblast collagenase inhibiti  
 C,Species: Mus musculus (house mouse)  
 C,Date: 05-Oct-1988 #sequence\_revision 12-Apr-1996 #text\_change 18-Jun-1999  
 C,Accession: A26917; A26106; A26633; A05276

R;Johnson, M.D.; Housey, G.M.; Kirschmeier, P.T.; Weinstein, I.B.  
Mol. Cell. Biol. 7, 2821-2829, 1987  
A:Title: Molecular cloning of gene sequences regulated by tumor promoters and mitogens  
A:Reference number: A26917; MUID:88038821; PMID:3670294  
A:Accession: A26917  
A:Molecule type: mRNA  
A:Residues: 1-205 <JOH>  
A:Cross-references: GB:M17243; NID:G202111; PIDN:AAA40471.1; PID:G202112  
A:Experimental source: embryonic fibroblast cDNA library  
R;Edwards, D.R.; Waterhouse, P.; Holman, M.L.; Denhardt, D.T.  
Nucleic Acids Res. 14, 8863-8878, 1986  
A:Title: A growth-responsive gene (16C8) in normal mouse fibroblasts homologous to a human p53.  
A:Reference number: A26106; MUID:87066763; PMID:3024122  
A:Accession: A26106  
A:Molecule type: mRNA  
A:Residues: 1-205 <EDW>  
A:Cross-references: GB:X04684; NID:G49702; PIDN:CNA28387.1; PID:G49704  
A:Experimental source: embryonic fibroblast cDNA library  
R;Gewirt, D.R.; Coulombe, B.; Castellino, M.; Skup, D.; Williams, B.R.G.  
EMBO J. 6, 651-657, 1987  
A:Title: Characterization and expression of a murine gene homologous to human EPA/TIMP.  
A:Reference number: A26633; MUID:87218524; PMID:3034603  
A:Accession: A26633  
A:Molecule type: DNA  
A:Residues: 1-51, 'R', '53-66', 'M', '67-116', 'KF', '119-120', 'N', '122-138', 'V', '140-142', 'KN', '144-193', 'S', '195-205', 'T', '206-210', 'L', '211-215', 'P', '216-220', 'G', '221-225', 'A', '226-230', 'C', '231-235', 'U', '236-240', 'G', '241-245', 'A', '246-250', 'C', '251-255', 'U', '256-260', 'G', '261-265', 'A', '266-270', 'C', '271-275', 'U', '276-280', 'G', '281-285', 'A', '286-290', 'C', '291-295', 'U', '296-300', 'G', '301-305', 'A', '306-310', 'C', '311-315', 'U', '316-320', 'G', '321-325', 'A', '326-330', 'C', '331-335', 'U', '336-340', 'G', '341-345', 'A', '346-350', 'C', '351-355', 'U', '356-360', 'G', '361-365', 'A', '366-370', 'C', '371-375', 'U', '376-380', 'G', '381-385', 'A', '386-390', 'C', '391-395', 'U', '396-400', 'G', '401-405', 'A', '406-410', 'C', '411-415', 'U', '416-420', 'G', '421-425', 'A', '426-430', 'C', '431-435', 'U', '436-440', 'G', '441-445', 'A', '446-450', 'C', '451-455', 'U', '456-460', 'G', '461-465', 'A', '466-470', 'C', '471-475', 'U', '476-480', 'G', '481-485', 'A', '486-490', 'C', '491-495', 'U', '496-500', 'G', '501-505', 'A', '506-510', 'C', '511-515', 'U', '516-520', 'G', '521-525', 'A', '526-530', 'C', '531-535', 'U', '536-540', 'G', '541-545', 'A', '546-550', 'C', '551-555', 'U', '556-560', 'G', '561-565', 'A', '566-570', 'C', '571-575', 'U', '576-580', 'G', '581-585', 'A', '586-590', 'C', '591-595', 'U', '596-600', 'G', '601-605', 'A', '606-610', 'C', '611-615', 'U', '616-620', 'G', '621-625', 'A', '626-630', 'C', '631-635', 'U', '636-640', 'G', '641-645', 'A', '646-650', 'C', '651-655', 'U', '656-660', 'G', '661-665', 'A', '666-670', 'C', '671-675', 'U', '676-680', 'G', '681-685', 'A', '686-690', 'C', '691-695', 'U', '696-700', 'G', '701-705', 'A', '706-710', 'C', '711-715', 'U', '716-720', 'G', '721-725', 'A', '726-730', 'C', '731-735', 'U', '736-740', 'G', '741-745', 'A', '746-750', 'C', '751-755', 'U', '756-760', 'G', '761-765', 'A', '766-770', 'C', '771-775', 'U', '776-780', 'G', '781-785', 'A', '786-790', 'C', '791-795', 'U', '796-800', 'G', '801-805', 'A', '806-810', 'C', '811-815', 'U', '816-820', 'G', '821-825', 'A', '826-830', 'C', '831-835', 'U', '836-840', 'G', '841-845', 'A', '846-850', 'C', '851-855', 'U', '856-860', 'G', '861-865', 'A', '866-870', 'C', '871-875', 'U', '876-880', 'G', '881-885', 'A', '886-890', 'C', '891-895', 'U', '896-900', 'G', '901-905', 'A', '906-910', 'C', '911-915', 'U', '916-920', 'G', '921-925', 'A', '926-930', 'C', '931-935', 'U', '936-940', 'G', '941-945', 'A', '946-950', 'C', '951-955', 'U', '956-960', 'G', '961-965', 'A', '966-970', 'C', '971-975', 'U', '976-980', 'G', '981-985', 'A', '986-990', 'C', '991-995', 'U', '996-1000', 'G', '1001-1005', 'A', '1006-1010', 'C', '1011-1015', 'U', '1016-1020', 'G', '1021-1025', 'A', '1026-1030', 'C', '1031-1035', 'U', '1036-1040', 'G', '1041-1045', 'A', '1046-1050', 'C', '1051-1055', 'U', '1056-1060', 'G', '1061-1065', 'A', '1066-1070', 'C', '1071-1075', 'U', '1076-1080', 'G', '1081-1085', 'A', '1086-1090', 'C', '1091-1095', 'U', '1096-1100', 'G', '1101-1105', 'A', '1106-1110', 'C', '1111-1115', 'U', '1116-1120', 'G', '1121-1125', 'A', '1126-1130', 'C', '1131-1135', 'U', '1136-1140', 'G', '1141-1145', 'A', '1146-1150', 'C', '1151-1155', 'U', '1156-1160', 'G', '1161-1165', 'A', '1166-1170', 'C', '1171-1175', 'U', '1176-1180', 'G', '1181-1185', 'A', '1186-1190', 'C', '1191-1195', 'U', '1196-1200', 'G', '1201-1205', 'A', '1206-1210', 'C', '1211-1215', 'U', '1216-1220', 'G', '1221-1225', 'A', '1226-1230', 'C', '1231-1235', 'U', '1236-1240', 'G', '1241-1245', 'A', '1246-1250', 'C', '1251-1255', 'U', '1256-1260', 'G', '1261-1265', 'A', '1266-1270', 'C', '1271-1275', 'U', '1276-1280', 'G', '1281-1285', 'A', '1286-1290', 'C', '1291-1295', 'U', '1296-1300', 'G', '1301-1305', 'A', '1306-1310', 'C', '1311-1315', 'U', '1316-1320', 'G', '1321-1325', 'A', '1326-1330', 'C', '1331-1335', 'U', '1336-1340', 'G', '1341-1345', 'A', '1346-1350', 'C', '1351-1355', 'U', '1356-1360', 'G', '1361-1365', 'A', '1366-1370', 'C', '1371-1375', 'U', '1376-1380', 'G', '1381-1385', 'A', '1386-1390', 'C', '1391-1395', 'U', '1396-1400', 'G', '1401-1405', 'A', '1406-1410', 'C', '1411-1415', 'U', '1416-1420', 'G', '1421-1425', 'A', '1426-1430', 'C', '1431-1435', 'U', '1436-1440', 'G', '1441-1445', 'A', '1446-1450', 'C', '1451-1455', 'U', '1456-1460', 'G', '1461-1465', 'A', '1466-1470', 'C', '1471-1475', 'U', '1476-1480', 'G', '1481-1485', 'A', '1486-1490', 'C', '1491-1495', 'U', '1496-1500', 'G', '1501-1505', 'A', '1506-1510', 'C', '1511-1515', 'U', '1516-1520', 'G', '1521-1525', 'A', '1526-1530', 'C', '1531-1535', 'U', '1536-1540', 'G', '1541-1545', 'A', '1546-1550', 'C', '1551-1555', 'U', '1556-1560', 'G', '1561-1565', 'A', '1566-1570', 'C', '1571-1575', 'U', '1576-1580', 'G', '1581-1585', 'A', '1586-1590', 'C', '1591-1595', 'U', '1596-1600', 'G', '1601-1605', 'A', '1606-1610', 'C', '1611-1615', 'U', '1616-1620', 'G', '1621-1625', 'A', '1626-1630', 'C', '1631-1635', 'U', 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'1911-1915', 'U', '1916-1920', 'G', '1921-1925', 'A', '1926-1930', 'C', '1931-1935', 'U', '1936-1940', 'G', '1941-1945', 'A', '1946-1950', 'C', '1951-1955', 'U', '1956-1960', 'G', '1961-1965', 'A', '1966-1970', 'C', '1971-1975', 'U', '1976-1980', 'G', '1981-1985', 'A', '1986-1990', 'C', '1991-1995', 'U', '1996-2000', 'G', '2001-2005', 'A', '2006-2010', 'C', '2011-2015', 'U', '2016-2020', 'G', '2021-2025', 'A', '2026-2030', 'C', '2031-2035', 'U', '2036-2040', 'G', '2041-2045', 'A', '2046-2050', 'C', '2051-2055', 'U', '2056-2060', 'G', '2061-2065', 'A', '2066-2070', 'C', '2071-2075', 'U', '2076-2080', 'G', '2081-2085', 'A', '2086-2090', 'C', '2091-2095', 'U', '2096-2100', 'G', '2101-2105', 'A', '2106-2110', 'C', '2111-2115', 'U', '2116-2120', 'G', '2121-2125', 'A', '2126-2130', 'C', '2131-2135', 'U', '2136-2140', 'G', '2141-2145', 'A', '2146-2150', 'C', '2151-2155', 'U', '2156-2160', 'G', '2161-2165', 'A', '2166-2170', 'C', '2171-2175', 'U', '2176-2180', 'G', '2181-2185', 'A', '2186-2190', 'C', '2191-2195', 'U', '2196-2200', 'G', '2201-2205', 'A', '2206-2210', 'C', '2211-2215', 'U', '2216-2220', 'G', '2221-2225', 'A', '2226-2230', 'C', '2231-2235', 'U', '2236-2240', 'G', '2241-2245', 'A', '2246-2250', 'C', '2251-2255', 'U', '2256-2260', 'G', '2261-2265', 'A', '2266-2270', 'C', '2271-2275', 'U', '2276-2280', 'G', '2281-2285', 'A', '2286-2290', 'C', '2291-2295', 'U', '2296-2300', 'G', '2301-2305', 'A', '2306-2310', 'C', '2311-2315', 'U', '2316-2320', 'G', '2321-2325', 'A', '2326-2330', 'C', '2331-2335', 'U', '2336-2340', 'G', '2341-2345', 'A', '2346-2350', 'C', '2351-2355', 'U', '2356-2360', 'G', '2361-2365', 'A', '2366-2370', 'C', '2371-2375', 'U', '2376-2380', 'G', '2381-2385', 'A', '2386-2390', 'C', '2391-2395', 'U', '2396-2400', 'G', '2401-2405', 'A', '2406-2410', 'C', '2411-2415', 'U', '2416-2420', 'G', '2421-2425', 'A', '2426-2430', 'C', '2431-2435', 'U', '2436-2440', 'G', '2441-2445', 'A', '2446-2450', 'C', '2451-2455', 'U', '2456-2460', 'G', '2461-2465', 'A', '2466-2470', 'C', '2471-2475', 'U', '2476-2480', 'G', '2481-2485', 'A', '2486-2490', 'C', '2491-2495', 'U', '2496-2500', 'G', '2501-2505', 'A', '2506-2510', 'C', '2511-2515', 'U', '2516-2520', 'G', '2521-2525', 'A', '2526-2530', 'C', '2531-2535', 'U', '2536-2540', 'G', '2541-2545', 'A', '2546-2550', 'C', '2551-2555', 'U', '2556-2560', 'G', '2561-2565', 'A', '2566-2570', 'C', '2571-2575', 'U', '2576-2580', 'G', '2581-2585', 'A', '2586-2590', 'C', '2591-2595', 'U', '2596-2600', 'G', '2601-2605', 'A', '2606-2610', 'C', '2611-2615', 'U', '2616-2620', 'G', '2621-2625', 'A', '2626-2630', 'C', '2631-2635', 'U', '2636-2640', 'G', '2641-2645', 'A', '2646-2650', 'C', '2651-2655', 'U', '2656-2660', 'G', '2661-2665', 'A', '2666-2670', 'C', '2671-2675', 'U', '2676-2680', 'G', '2681-2685', 'A', '2686-2690', 'C', '2691-2695', 'U', '2696-2700', 'G', '2701-2705', 'A', '2706-2710', 'C', '2711-2715', 'U', '2716-2720', 'G', '2721-2725', 'A', '2726-2730', 'C', '2731-2735', 'U', '2736-2740', 'G', '2741-2745', 'A', '2746-2750', 'C', '2751-2755', 'U', '2756-2760', 'G', '2761-2765', 'A', '2766-2770', 'C', '2771-2775', 'U', '2776-2780', 'G', '2781-2785', 'A', '2786-2790', 'C', '2791-2795', 'U', '2796-2800', 'G', '2801-2805', 'A', '2806-2810', 'C', '2811-2815', 'U', '2816-2820', 'G', '2821-2825', 'A', '2826-2830', 'C', '2831-2835', 'U', '2836-2840', 'G', '2841-2845', 'A', '2846-2850', 'C', '2851-2855', 'U', '2856-2860', 'G', '2861-2865', 'A', '2866-2870', 'C', '2871-2875', 'U', '2876-2880', 'G', '2881-2885', 'A', '2886-2890', 'C', '2891-2895', 'U', '2896-2900', 'G', '2901-2905', 'A', '2906-2910', 'C', '2911-2915', 'U', '2916-2920', 'G', '2921-2925', 'A', '2926-2930', 'C', '2931-2935', 'U', '2936-2940', 'G', '2941-2945', 'A', '2946-2950', 'C', '2951-2955', 'U', '2956-2960', 'G', '2961-2965', 'A', '2966-2970', 'C', '2971-2975', 'U', '2976-2980', 'G', '2981-2985', 'A', '2986-2990', 'C', '2991-2995', 'U', '2996-3000', 'G', '3001-3005', 'A', '3006-3010', 'C', 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'3286-3290', 'C', '3291-3295', 'U', '3296-3300', 'G', '3301-3305', 'A', '3306-3310', 'C', '3311-3315', 'U', '3316-3320', 'G', '3321-3325', 'A', '3326-3330', 'C', '3331-3335', 'U', '3336-3340', 'G', '3341-3345', 'A', '3346-3350', 'C', '3351-3355', 'U', '3356-3360', 'G', '3361-3365', 'A', '3366-3370', 'C', '3371-3375', 'U', '3376-3380', 'G', '3381-3385', 'A', '3386-3390', 'C', '3391-3395', 'U', '3396-3400', 'G', '3401-3405', 'A', '3406-3410', 'C', '3411-3415', 'U', '3416-3420', 'G', '3421-3425', 'A', '3426-3430', 'C', '3431-3435', 'U', '3436-3440', 'G', '3441-3445', 'A', '3446-3450', 'C', '3451-3455', 'U', '3456-3460', 'G', '3461-3465', 'A', '3466-3470', 'C', '3471-3475', 'U', '3476-3480', 'G', '3481-3485', 'A', '3486-3490', 'C', '3491-3495', 'U', '3496-3500', 'G', '3501-3505', 'A', '3506-3510', 'C', '3511-3515', 'U', '3516-3520', 'G', '3521-3525', 'A', '3526-3530', 'C', '3531-3535', 'U', '3536-3540', 'G', '3541-3545', 'A', '3546-3550', 'C', '3551-3555', 'U', '3556-3560', 'G', 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'3836-3840', 'G', '3841-3845', 'A', '3846-3850', 'C', '3851-3855', 'U', '3856-3860', 'G', '3861-3865', 'A', '3866-3870', 'C', '3871-3875', 'U', '3876-3880', 'G', '3881-3885', 'A', '3886-3890', 'C', '3891-3895', 'U', '3896-3900', 'G', '3901-3905', 'A', '3906-3910', 'C', '3911-3915', 'U', '3916-3920', 'G', '3921-3925', 'A', '3926-3930', 'C', '3931-3935', 'U', '3936-3940', 'G', '3941-3945', 'A', '3946-3950', 'C', '3951-3955', 'U', '3956-3960', 'G', '3961-3965', 'A', '3966-3970', 'C', '3971-3975', 'U', '3976-3980', 'G', '3981-3985', 'A', '3986-3990', 'C', '3991-3995', 'U', '3996-4000', 'G', '4001-4005', 'A', '4006-4010', 'C', '4011-4015', 'U', '4016-4020', 'G', '4021-4025', 'A', '4026-4030', 'C', '4031-4035', 'U', '4036-4040', 'G', '4041-4045', 'A', '4046-4050', 'C', '4051-4055', 'U', '4056-4060', 'G', '4061-4065', 'A', '4066-4070', 'C', '4071-4075', 'U', '4076-4080', 'G', '4081-4085', 'A', '4086-4090', 'C', '4091-4095', 'U', '4096-4100', 'G', '4101-4105', 'A', '4106-4110', 'C', '4111-4115', 'U', '4116-4120', 'G', '4121-4125', 'A', '4126-4130', 'C', '4131-4135', 'U', '4136-4140', 'G', '4141-4145', 'A', '4146-4150', 'C', '4151-4155', 'U', '4156-4160', 'G', '4161-4165', 'A', '4166-4170', 'C', '4171-4175', 'U', '4176-4180', 'G', '4181-4185', 'A', '4186-4190', 'C', '4191-4195', 'U', '4196-4200', 'G', '4201-4205', 'A', '4206-4210', 'C', '4211-4215', 'U', '4216-4220', 'G', '4221-4225', 'A', '4226-4230', 'C', '4231-4235', 'U', '4236-4240', 'G', '4241-4245', 'A', '4246-4250', 'C', '4251-4255', 'U', '4256-4260', 'G', '4261-4265', 'A', '4266-4270', 'C', '4271-4275', 'U', '4276-4280', 'G', '4281-4285', 'A', '4286-4290', 'C', '4291-4295', 'U', '4296-4300', 'G', '4301-4305', 'A', '4306-4310', 'C', '4311-4315', 'U', '4316-4320', 'G', '4321-4325', 'A', '4326-4330', 'C', '4331-4335', 'U', '4336-4340', 'G', '4341-4345', 'A', '4346-4350', 'C', '4351-4355', 'U', '4356-4360', 'G', '4361-4365', 'A', '4366-4370', 'C', '4371-4375', 'U', '4376-4380', 'G', '4381-4385', 'A', 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J. Biol. Chem. 264, 17374-17378, 1989  
 A>Title: Tissue inhibitor of metalloproteinase (TIMP-2). A new member of the metalloprote  
 A:Reference number: A34464; MUID:90008902; PMID:2793861  
 A:Accession: A34464  
 A:Molecule type: protein  
 A:Residues: 27-77, 'K', '79-81, 'I', '83-100, 'E', '102-117, '119-121, 'R', '123-149, 'Q', '151-174, 'T', '1  
 A:Experimental source: serum-free culture medium of A2058 cells  
 R:Goldberg, G.I.; Warner, B.L.; Grant, G.A.; Eissen, A.Z.; Wilhelm, S.; He, C.  
 Proc. Natl. Acad. Sci. U.S.A. 86, 8207-8211, 1989  
 A>Title: Human 72-kilodalton type IV collagenase forms a complex with a tissue inhibitor  
 A:Reference number: A34415; MUID:90046765; PMID:2554304  
 A:Accession: A34415  
 A:Molecule type: protein  
 A:Residues: 30-51, '124-141, '159-173 <COL>  
 R:Malik, K.; Sejima, H.; Aoki, T.; Iwata, K.  
 submitted to the EMBL Data Library, August 1990  
 A:Description: Nucleotide sequence of a TIMP-II cDNA.  
 A:Reference number: S21303  
 A:Accession: S21303  
 A:Molecule type: mRNA  
 A:Residues: 30-95, 'V', '97-214 <MAL>  
 A:Cross-references: EMBL:X54533; NID:937180; PIDN:CA38400.1; PID:G37181  
 R:Osthus, A.; Knauper, V.; Oberhoff, R.; Reinke, H.; Tschesche, H.  
 FEBS Lett. 296, 16-20, 1992  
 A>Title: Isolation and characterization of tissue inhibitors of metalloproteinases (TIMP  
 A:Reference number: S20318; MUID:92111776; PMID:1730286  
 A:Accession: S20318  
 A:Molecule type: protein  
 A:Residues: 'X', '28, 'X', '30-38, 'X', '40-41 <OST>  
 A:Experimental source: rheumatoid synovial fluid  
 R:Ward, R.V.; Hemby, R.M.; Reynolds, J.J.; Murphy, G.  
 Biochem. J. 278, 179-187, 1991  
 A>Title: The purification of tissue inhibitor of metalloproteinases-2 from its 72 kDa pr  
 A:Reference number: S17165; MUID:91354200; PMID:1909113  
 A:Accession: S17165  
 A:Molecule type: preliminary  
 A:Status: preliminary  
 A:Residues: 27, 'X', '29, 'X', '31-38 <WAR>  
 R:Ohba, Y.; Goto, Y.; Kimura, Y.; Suzuki, F.; Hisa, T.; Takahashi, K.; Takigawa, M.  
 Biochim. Biophys. Acta 1245, 1-8, 1995  
 A>Title: Purification of an angiogenesis inhibitor from culture medium conditioned by a  
 A:Reference number: S58794; MUID:9533380; PMID:754625  
 A:Accession: S58794  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 27-37 <OHBA>  
 C:Genetics:  
 A:Gene: GDB:TIMP2  
 A:Cross-references: GDB:132612; OMIM:188825  
 A:Map position: 17q25-17q25  
 A:Function:  
 A:Description: regulation of extracellular matrix remodeling by inhibition of matrix met  
 possibly controlling their activation; TIMP-1 and TIMP-2 possess erythroid potentiating  
 C:Superfamily: metalloproteinase inhibitor  
 C:Keywords: erythropoiesis; extracellular matrix; metalloproteinase inhibitor; mitogen  
 F.1-26/Domains: signal sequence #status predicted <SIG>  
 F.27-220/Product: metalloproteinase inhibitor 2 #status experimental <MAT>  
 F.27-98, '29-127, '39-152, '154-201, '159-164, '172-193/Disulfide bonds: #status predicted

Query Match 40.4%; Score 234; DB 1; Length 220;  
 Best Local Similarity 44.7%; Pred. No. 7, 2e-19;  
 Matches 51; Conservative 15; Mismatches 34; Indels 14; Gaps 5;

OY 1 CTCVPHPOTACNSDLVIRAKFVGTPEVNO-TTLYO-----RYEIKMTKMYKGFQALG 53  
 DB 27 CSCSPVHPQACNADVIRAKVSEKVEDSNDYGNPKIQYEIFQIKMKF-----G 81

OY 54 DADIRFVYTPMESVCGYFHRSHNRSEFLLAGKQ-DGLHITTCSPVAPWN 106  
 DB 82 PKDIEFITYTASSAVCG-VSLDVGKKEYLLAGKAGDGKMHITLCDFIVPD 134

RESULT 10

S38624  
 metalloproteinase inhibitor 2 precursor - long-tailed hamster (fragment)  
 N:Alternate names: TIMP-2; tissue inhibitor of metalloproteinases 2  
 C:Species: Cricetus longicaudatus (long-tailed hamster)  
 C>Date: 06-Jan-1995 #sequence\_revision 12-Apr-1996 #text\_change 18-Jun-1999  
 C:Accession: S38624  
 R:Suzuki, Y.  
 submitted to the EMBL Data Library, November 1993  
 A:Reference number: S38624  
 A:Accession: S38624  
 A:Molecule type: mRNA  
 A:Residues: 1-196 <SUZ>  
 A:Cross-references: EMBL:X75924; NID:9414876; PIDN:CA53528.1; PID:G414877  
 A:Function:  
 A:Description: regulation of extracellular matrix remodeling by inhibition of matrix met  
 possibly controlling their activation; TIMP-1 and TIMP-2 possess erythroid potentiating  
 C:Superfamily: metalloproteinase inhibitor  
 C:Keywords: erythropoiesis; extracellular matrix; metalloproteinase inhibitor; mitogen  
 F.3-196/Product: metalloproteinase inhibitor 2 #status predicted <MAT>  
 F.3-74, '5-103, '15-128, '130-177, '135-140, '148-169/Disulfide bonds: #status predicted

Query Match 40.2%; Score 233; DB 1; Length 196;  
 Best Local Similarity 44.7%; Pred. No. 8, 2e-19;  
 Matches 51; Conservative 15; Mismatches 34; Indels 14; Gaps 5;

OY 1 CTCVPHPOTACNSDLVIRAKFVGTPEVNO-TTLYO-----RYEIKMTKMYKGFQALG 53  
 DB 3 CSCSPVHPQACNADVIRAKVSEKVEDSNDYGNPKIQYEIFQIKMKF-----G 57

OY 54 DADIRFVYTPMESVCGYFHRSHNRSEFLLAGKQ-DGLHITTCSPVAPWN 106  
 DB 58 PKDIEFITYTASSAVCG-VSLDVGKKEYLLAGKAGDGKMHITLCDFIVPD 110

RESULT 11

JH0683  
 metalloproteinase inhibitor 2 precursor - mouse  
 N:Alternate names: TIMP-2; tissue inhibitor of metalloproteinases 2  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C:Accession: JH0683; JCI1234; S18428; S15987; S26189  
 R:Shimizu, S.; Malik, K.; Sejima, H.; Kishii, J.; Hayakawa, T.; Koiwai, O.  
 Gene 114, 291-292, 1992  
 A>Title: Cloning and sequencing of the cDNA encoding a mouse tissue inhibitor of metallo  
 A:Reference number: JH0683; MUID:92290292; PMID:1603312  
 A:Accession: JH0683  
 A:Molecule type: mRNA  
 A:Residues: 1-220 <SHI>  
 A:Cross-references: EMBL:X62622; NID:954801; PIDN:CAA44491.1; PID:954802  
 A:Experimental source: 3T3 fibroblast strain Balb/c  
 R:Leeco, K.U.; Hayden, L.U.; Sharma, R.R.; Rocheteau, H.; Greenberg, A.H.; Edwards, D.R.  
 Gene 117, 209-217, 1992  
 A>Title: Differential regulation of TIMP-1 and TIMP-2 mRNA expression in normal and Ha-r  
 A:Reference number: JCI1234; MUID:92347695; PMID:1639268  
 A:Accession: JCI1234  
 A:Molecule type: mRNA  
 A:Residues: 1, '11, 'H', '13-20, 'L', '22-194, 'E', '196-220 <LEC>  
 A:Cross-references: GB:M93954; NID:9202053; PIDN:AAA40446.1; PID:9202054  
 R:Kishii, J.  
 Matrix 11, 373, 1991  
 A>Title: Correction.  
 A:Reference number: S18428; MUID:92244125; PMID:1667327  
 A:Accession: S18428  
 A:Molecule type: protein  
 A:Residues: 27-46, 'H', '48-50-53, 'VD', '56, 'DY' <KIS>  
 R:Kishii, J.I.; Ogawa, K.; Yamamoto, S.; Hayakawa, T.  
 Matrix 11, 10-16, 1991  
 A>Title: Purification and characterization of a new tissue inhibitor of metalloproteinase  
 A:Reference number: S15987; MUID:91226375; PMID:1851244  
 A:Accession: S15987  
 A:Molecule type: protein  
 A:Residues: 27-46, 'HLX', '50-52, 'LX', '55-56, 'DXX', '60, 'X', '62 <KIS>  
 A>Note: this sequence has been revised in reference S18428



Job time : 11.6 secs

C:Function:  
A:Description: regulation of extracellular matrix remodeling by inhibition of matrix metalloproteinase inhibitor  
C:Superfamily: metalloproteinase inhibitor  
C:Keywords: erythropoiesis; extracellular matrix; metalloproteinase inhibitor; mitogen  
F:1-26/Domain: signal sequence #status predicted <SIG>  
F:27-220/Product: metalloproteinase inhibitor 2 #status predicted <MAT>  
F:27-98,29-139,152,154-201,159-164,172-193/Disulfide bonds: #status predicted

Query Match 39.2%; Score 227; DB 1; Length 220;  
Best Local Similarity 43.9%; Pred. No. 4,5e-18;  
Matches 50; Conservative 16; Mismatches 34; Indels 14; Gaps 5;

QY 1 CTCVPPHQTAFNCNSDLVIRAKVGTPEVNO-TTLVQ-----RYEIKMTKMYKGFQALG 53  
DB 27 CSCSPVHPQOACNCDIVIRAKVKNKEVDGNDIYGNPKRIQYIKQIKMFK-----G 81  
QY 54 DAADIRFYTPMESVCGYFRSHNRSEFLIAGKIQ-DGLIHITTCGFVAPWN 106  
DB 82 PDQIEFYTPAPAAVCG-VSLDIGGKEYLIAGKAGNGNMHITLCPDIPVWD 134

## RESULT 15

A43429  
metalloproteinase inhibitor 3 precursor - chicken  
N:Alternate names: 21K extracellular matrix protein; TIMP-3; tissue inhibitor of metalloproteinase  
C:Species: Gallus gallus (chicken)  
C:Date: 04-Mar-1993 #sequence\_revision 12-Apr-1996 #text\_change 18-Jun-1999  
C:Accession: A43429; A39043  
R:Pavloff, N.; Staskus, P.W.; Kishnani, N.S.; Hawkes, S.P.  
J. Biol. Chem. 267, 17321-17326, 1992  
A:Title: A new inhibitor of metalloproteinases from chicken: ChIMP-3. A third member of the TIMP family  
A:Reference number: A43429; MUID:92381050; PMID:1512267  
A:Accession: A43429

A:Molecule type: mRNA  
A:Residues: 1-212 <PAV>

A:Cross-references: GB:M94531; NID:G211901; PIDN:AAA48813.1; PID:G211902

A:Experimental source: ten-day old embryo cDNA library

A>Note: Sequence extracted from NCBI backbone (NCBIN:111960, NCBIPI:111961)

R:Staskus, P.W.; Maslusz, F.R.; Pallanck, L.J.; Hawkes, S.P.  
J. Biol. Chem. 266, 449-454, 1991

A:Title: The 21-kDa protein is a transformation-sensitive metalloproteinase inhibitor of

A:Reference number: A39043; MUID:91093162; PMID:1845973

A:Accession: A39043

A:Molecule type: protein

A:Residues: 26-51, 'I', 53 <STR>

A:Experimental source: cultured embryonic fibroblasts infected with Rous sarcoma virus

A>Note: contains disulfide bonds; not glycosylated; has inhibitory activity

C:Function:  
A:Description: regulation of extracellular matrix remodeling by inhibition of matrix metalloproteinase inhibitor  
A>Note: TIMP-1 and TIMP-3 have distinct but overlapping tissue-specific expression patterns

C:Superfamily: metalloproteinase inhibitor

C:Keywords: extracellular matrix; glycoprotein; metalloproteinase inhibitor

F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-212/Product: metalloproteinase inhibitor 3 #status experimental <MAT>

F:25-92,27-119,37-144,146-193,151-156,164-185/Disulfide bonds: #status predicted

F:208/Binding site: carbohydrate (asn) (covalent) #status absent

Query Match 37.7%; Score 218; DB 1; Length 212;  
Best Local Similarity 40.2%; Pred. No. 4,5e-17;  
Matches 43; Conservative 21; Mismatches 37; Indels 6; Gaps 3;

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DB 25 CTCVPIHPQDACNSDIVIRAKVGNKEVDGNDIYGNPKRIQYIKQIKMFK-----G 81

QY 60 FVYTPAMESVCGYFRSHNRSEFLIAGKIQDGLIHITTCGFVAPWN 106  
DB 82 YITPASESLCGV--KLEVNKQYILITGRVGEKQYITGLCNMYEKMD 126

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OM protein - protein search, using sw model

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(without alignments)  
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Perfect score: 579  
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Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	579	100.0	207	1	TIM1_HUMAN
2	579	100.0	207	1	TIM1_PAPCY
3	569	98.3	207	1	TIM1_MACMU
4	508	87.7	207	1	TIM1_BOVIN
5	507	87.6	206	1	TIM1_RABIT
6	504	87.0	207	1	TIM1_SHEEP
7	500	86.4	207	1	TIM1_FIG
8	477	82.4	207	1	TIM1_HORSE
9	458	79.1	205	1	TIM1_MOUSE
10	455	78.6	207	1	TIM1_CANFA
11	446	77.0	217	1	TIM1_RAT
12	235	40.6	214	1	TIM3_SCYTO
13	234	40.4	220	1	TIM2_CAVPO
14	234	40.4	220	1	TIM2_HUMAN
15	233	40.2	196	1	TIM2_CRILLO
16	233	40.2	220	1	TIM2_MOUSE
17	233	40.2	220	1	TIM2_RAT
18	229	38.6	220	1	TIM2_CANFA
19	228	38.4	194	1	TIM2_RABIT
20	227	39.2	220	1	TIM2_BOVIN
21	219	37.8	220	1	TIM2_CHICK
22	218	37.7	212	1	TIM3_CHICK
23	215	37.1	211	1	TIM3_HORSE
24	215	37.1	211	1	TIM3_HUMAN
25	213	36.8	214	1	TIM3_XENLA
26	212	36.6	211	1	TIM3_MOUSE
27	212	36.6	211	1	TIM3_RAT
28	210.5	36.4	224	1	TIM4_MOUSE
29	210	36.3	211	1	TIM4_BOVIN
30	208.5	36.0	224	1	TIM4_RAT
31	201.5	34.8	224	1	TIM4_HUMAN
32	155	26.8	151	1	TIM3_RABIT
33	140.5	24.3	107	1	TIM4_BOVIN

34	140.5	24.3	170	1	TIM4_RABIT	097591 oryctolagus
35	137.5	23.7	91	1	TIM2_HORSE	077117 equus caball
36	100	17.3	210	1	TIMP_DROME	09vhl4 drosophila
37	69	11.9	345	1	APOH_MOUSE	001339 mus musculus
38	67.5	11.7	421	1	NXP2_CABEL	09xv88 caenorhabdi
39	66	11.4	572	1	DPY2_BOVIN	002675 bos taurus
40	66	11.4	572	1	DPY2_HUMAN	016555 homo sapien
41	65	11.2	2549	1	FRAP_MOUSE	09j1n9 mus musculus
42	65	11.2	2549	1	FRAP_RAT	P42346 rattus norv
43	64.5	11.1	1005	1	BGAL_ACTPL	P70753 actinobacill
44	64	11.1	187	1	ATPD_ODOSI	Q00821 odontocella s
45	63.5	11.0	352	1	RECF_TREPA	083049 treponema p

## ALIGNMENTS

RESULT 1  
ID TIM1\_HUMAN STANDARD; PRT; 207 AA.  
AC P01033; 014252; 09UCU1.  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Metalloproteinase inhibitor 1 precursor (TIMP-1) (Erythroid  
potentiating activity) (EPA) (Tissue inhibitor of metalloproteinases)  
DE (Fibroblast collagenase inhibitor) (Collagenase inhibitor).  
GN TIMP1 OR TIMP OR CLGI.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=86040463; PubMed=3903517;  
RA Docherty A.J.P., Lyons A., Smith B.J., Wright E.M., Stephens P.E.,  
RA Harris T.J.R., Murphy G., Reynolds J.J.;  
RT "Sequence of human tissue inhibitor of metalloproteinases and its  
RT identity to erythroid-potentiating activity.";  
RL Nature 318:66-69(1985).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85240567; PubMed=3839290;  
RA Gasson J.C., Golde D.W., Kaufman S.E., Westbrook C.A., Hewick R.M.,  
RA Kauffman R.J., Wong G.G., Temple P.A., Leary A.C., Brown E.L.,  
RA Orr E.C., Clark S.C.;  
RT "Molecular characterization and expression of the gene encoding human  
RT erythroid-potentiating activity.";  
RL Nature 315:768-771(1985).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=86205964; PubMed=3010309;  
RA Carmichael D.F., Sommer A., Thompson R.C., Anderson D.C., Smith C.G.,  
RA Welgus H.G., Stricklin G.P.;  
RT "Primary structure and cDNA cloning of human fibroblast collagenase  
RT inhibitor.";  
RL Proc. Natl. Acad. Sci. U.S.A. 83:2407-2411(1986).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX Kaczorek M., Honore N., Ribes V., Dehoux P., Cornet P., Cartwright T.,  
RA Stacek R.E.;  
RT "Molecular cloning and synthesis of biologically active human tissue  
RT inhibitor of metalloproteinases in yeast.";  
RL Biotechnology 5:595-598(1987).  
RN [5]  
RP SEQUENCE FROM N.A.  
RX TISSUE=Ovary;  
MEDLINE=91025550; PubMed=2171551;  
RA Rapp G., Freudenstein J., Klaudiny J., Mucha J., Wempe F., Zimmer M.,  
RA Scheit K.H.;  
RT "Characterization of three abundant mRNAs from human ovarian  
RL granulosa cells.";  
RL DNA Cell Biol. 9:479-485(1990).

RN [6] SEQUENCE FROM N.A.  
RP MEDLINE=94123576; PubMed=7507419;  
RA Oprook A., Kenney M.C., Brown D.;  
RT "Characterization of a human corneal metalloproteinase inhibitor  
RT (TIMP-1).";  
RL Curr. Eye Res. 12:877-883(1993).  
RN [7]  
RP SEQUENCE FROM N.A.  
RP TISSUE=Cervix;  
RA Strausberg R.;  
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
RN [8]  
RP SEQUENCE OF 42-207 FROM N.A.  
RA Matsuda T., Kohno K., Kuwano M.;  
RL Submitted (JUL-1992) to the EMBL/GenBank/DBJ databases.  
RN [9]  
RP SEQUENCE OF 1-40 FROM N.A.  
RA Hardcastle A.J.;  
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.  
RN [10]  
RP DISULFIDE BONDS, AND PARTIAL SEQUENCE.  
RX MEDLINE=90303199; PubMed=2163605;  
RA Williamson R.A., Matson F.A.O., Angal S., Koklitis P., Panico M.,  
RA Morris H.R., Carne A.F., Smith B.J., Harris T.J.R., Freedman R.B.;  
RT "Disulphide bond assignment in human tissue inhibitor of  
RT metalloproteinases (TIMP).";  
RL Biochem. J. 268:267-274(1990).  
RN [11]  
RP SEQUENCE OF 24-38.  
RC TISSUE=Synovial fluid;  
RX MEDLINE=92111776; PubMed=1730286;  
RA Oshues A., Knauper V., Oberhoff R., Reinke H., Tschesche H.;  
RT "Isolation and characterization of tissue inhibitors of  
RT metalloproteinases (TIMP-1 and TIMP-2) from human rheumatoid synovial  
RT fluid.";  
RL FEBS Lett. 296:16-20(1992).  
RN [12]  
RP SEQUENCE OF 24-52.  
RX MEDLINE=91355647; PubMed=1653055;  
RA Van Ranst M., Norga K., Masure S., Proost P., Vandekerckhove F.,  
RA Auwerx J., Van Damme J., Odenakker G.;  
RT "The cytokine-protease connection: identification of a 96-kD TIMP-1  
RT gelatinase and regulation by interleukin-1 and cytokine inducers.";  
RL Cytokine 3:231-239(1991).  
RN [13]  
RP MUTAGENESIS.  
RX MEDLINE=93041700; PubMed=1420137;  
RA O'Shea M., Willenbrock F., Williamson R.A., Cockett M.I.,  
RA Freedman R.B., Reynolds J.J., Docherty A.J.P., Murphy G.;  
RT "Site-directed mutations that alter the inhibitory activity of the  
RT tissue inhibitor of metalloproteinases-1: importance of the  
RT N-terminal region between cysteine 3 and cysteine 13.";  
RL Biochemistry 31:10146-10152(1992).  
RN [14]  
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF COMPLEX WITH MMP-3.  
RX MEDLINE=97433330; PubMed=9288970;  
RA Gomis-Ruth F.X., Maskos K., Betz M., Bergner A., Huber R., Suzuki K.,  
RA Yoshida N., Nagase H., Brew K., Bourenkov G.P., Bartunik H., Bode W.;  
RT "Mechanism of inhibition of the human matrix metalloproteinase  
RT stromelysin-1 by TIMP-1.";  
RL Nature 389:77-81(1997).  
RN [15]  
RP STRUCTURE BY NMR OF 24-149.  
RX MEDLINE=20090931; PubMed=10623524;  
RA Wu B., Arumugam S., Gao G., Lee G.I., Semchenko V., Huang W.,  
RA Brew K., Van Doren S.R.;  
RT "NMR structure of tissue inhibitor of metalloproteinases-1 implicates  
RT localized induced fit in recognition of matrix metalloproteinases.";  
RL J. Mol. Biol. 295:257-268(2000).  
CC -!- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)  
CC AND IRREVERSIBLY INACTIVATES THEM. ALSO MEDIATES ERYTHROPOIESIS IN  
CC VITRO; BUT, UNLIKE IL-3, IT IS SPECIES-SPECIFIC, STIMULATING THE

CC GROWTH AND DIFFERENTIATION OF ONLY HUMAN AND MURINE ERYTHROID  
CC PROGENITORS. KNOWN TO ACT ON MMP-1, MMP-2, MMP-3, MMP-7, MMP-8,  
CC MMP-9, MMP-10, MMP-11, MMP-12, MMP-13 AND MMP-16. DOES NOT ACT ON  
CC MMP-14.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- PTM: THE ACTIVITY OF TIMP-1 IS DEPENDENT ON THE PRESENCE OF  
CC DISULFIDE BONDS.  
CC -!- SIMILARITY: BELONGS TO THE TIMP FAMILY.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; X03124; CAA26902.1; -  
CC EMBL; M12670; AAA52436.1; -  
CC EMBL; X02598; CAA26443.1; -  
CC EMBL; M59906; AAA63234.1; -  
CC EMBL; S68252; AAD14009.1; -  
CC EMBL; BC000866; AAH00866.1; -  
CC EMBL; D11139; BAA01913.1; -  
CC EMBL; L47361; BAA75558.1; -  
CC EMBL; A10416; CAA00898.1; -  
CC PIR; A01269; ZYHUEP.  
CC PIR; A23534; A23534.  
CC PIR; A35826; A35826.  
CC PDB; 1UEA; 25-NOV-98.  
CC PDB; 1D2B; 22-DEC-99.  
CC GlycoSuiteDB; P01033; -  
CC Genew; HGNC:11820; TIMP1.  
CC MIM; 305370; -  
CC InterPro; IPR001820; TIMP.  
CC Pfam; PF00965; TIMP; 1.  
CC SMART; SMO0206; TIMP; 1.  
CC PROSITE; PS00288; TIMP; 1.  
CC KW Glycoprotein; Metalloprotease inhibitor; Erythrocyte maturation;  
CC 3D-structure; Signal.  
CC FT SIGNAL 1 23 METALLOPROTEINASE INHIBITOR 1.  
FT CHAIN 24 207  
FT DISULFID 26 122  
FT DISULFID 36 147  
FT DISULFID 150 197  
FT DISULFID 155 160  
FT DISULFID 168 189  
FT CARBOHYD 53 53  
FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .).  
FT CONFLICT 23 23 /FTID=CAR\_000002.  
FT CONFLICT 44 44 N-LINKED (GLCNAC. . .).  
FT CONFLICT 207 207 A -> P (IN REF. 2).  
FT CONFLICT 207 207 A -> P (IN REF. 8).  
SQ SEQUENCE 207 AA; 23171 MW; 5AB4F90FFAB2ECDC CRC64;  
Query Match 100.0%; Score 579; DB 1; Length 207;  
Best Local Similarity 100.0%; Pred. No. 2.5e-59;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CTCVPPHPQTAFNCSDLVIRAKFVGTPEVNTTLYQRYEIKMTKMYKGFQALGDAADIRF 60  
Db 24 CTCVPPHPQTAFNCSDLVIRAKFVGTPEVNTTLYQRYEIKMTKMYKGFQALGDAADIRF 83  
Qy 61 VYTPAMESVCCGYFRRSHNRSEFLIAGKLDGLLHITTCSEFVAPWN 106  
Db 84 VYTPAMESVCCGYFRRSHNRSEFLIAGKLDGLLHITTCSEFVAPWN 129  
RESULT 2  
TIM1\_PAPCY STANDARD; PRT; 207 AA.  
ID -TIM1\_PAPCY



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AC PA9061;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Metalloproteinase inhibitor 1 precursor (TIMP-1).
GN TIMP1.
OS Papio cynocephalus (Yellow baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Papio.
OX NCBI_TaxID=9556;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Arteria;
RX MEDLINE=96011646; PubMed=7590279;
RA Forough R., Nikkari S.T., Hasenstab D., Lea H., Clowers A.W.;
RT "Cloning and characterization of a cDNA encoding the baboon tissue
inhibitor of matrix metalloproteinase-1 (TIMP-1).";
R Gene 163:267-271(1995).
CC -1- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
AND IRREVERSIBLY INACTIVATES THEM.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: THE ACTIVITY OF TIMP-1 IS DEPENDENT ON THE PRESENCE OF
DISULFIDE BONDS.
CC -1- SIMILARITY: BELONGS TO THE TIMP FAMILY.
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CC -----
DR EMBL; L37295; AAA99943.1; -
DR HSSP; P01033; ID2B.
DR InterPro; IPR001820; TIMP.
DR Pfam; PF00965; TIMP; 1.
DR SMART; SMO0206; TIMP; 1.
DR PROSITE; PS00288; TIMP; 1.
KW Glycoprotein; Metalloproteinase inhibitor; Erythrocyte maturation;
KW Signal.
FT CHAIN 1 23 BY SIMILARITY.
FT SIGNAL 1 23 METALLOPROTEINASE INHIBITOR 1.
FT DISULFID 24 207 BY SIMILARITY.
FT DISULFID 26 122 BY SIMILARITY.
FT DISULFID 36 147 BY SIMILARITY.
FT DISULFID 150 197 BY SIMILARITY.
FT DISULFID 155 160 BY SIMILARITY.
FT DISULFID 168 189 BY SIMILARITY.
FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 207 AA; 23213 MW; 5AE4FBDEAB2BCDC CRC64;
Query Match 100.0%; Score 579; DB 1; Length 207;
Best Local Similarity 100.0%; Pred. No. 2.5e-59;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTCVPPHPOTACNSDLVIRAKVGTPEVNOPTLLYQRYEIKTKMYKGFQALGDAADIRF 60
DB 24 CTCVPPHPOTACNSDLVIRAKVGTPEVNOPTLLYQRYEIKTKMYKGFQALGDAADIRF 83
QY 61 VYTPMESVCGYFHRSHNRSEFLIAGKLODGLIHITTCSPFAPWN 106
DB 84 VYTPMESVCGYFHRSHNRSEFLIAGKLODGLIHITTCSPFAPWN 129
RESULT 3
ID TIM1_MACMU STANDARD; PRT; 207 AA.
AC Q95KL9;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)

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DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Metalloproteinase inhibitor 1 precursor (TIMP-1).
GN TIMP1.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Ji S., Wang Y., Li H., Ji W., Piao Y.;
RT "Cloning and characterization of tissue inhibitor of matrix
metalloproteinase-1 (TIMP-1) cDNA from Macaca mulatta.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
AND IRREVERSIBLY INACTIVATES THEM.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: THE ACTIVITY OF TIMP-1 IS DEPENDENT ON THE PRESENCE OF
DISULFIDE BONDS.
CC -1- SIMILARITY: BELONGS TO THE TIMP FAMILY.
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CC -----
DR EMBL; AF366397; AAK53704.1; -
DR InterPro; IPR001820; TIMP.
DR Pfam; PF00965; TIMP; 1.
DR PROSITE; PS00288; TIMP; FALSE_NEG.
KW Glycoprotein; Metalloproteinase inhibitor; Erythrocyte maturation;
KW Signal.
FT CHAIN 1 23 BY SIMILARITY.
FT SIGNAL 1 23 METALLOPROTEINASE INHIBITOR 1.
FT DISULFID 24 207 BY SIMILARITY.
FT DISULFID 26 122 BY SIMILARITY.
FT DISULFID 36 147 BY SIMILARITY.
FT DISULFID 150 197 BY SIMILARITY.
FT DISULFID 155 160 BY SIMILARITY.
FT DISULFID 168 189 BY SIMILARITY.
FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 207 AA; 23247 MW; 4EE227D2AAB8580 CRC64;
Query Match 98.3%; Score 569; DB 1; Length 207;
Best Local Similarity 99.1%; Pred. No. 3.6e-58;
Matches 105; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CTCVPPHPOTACNSDLVIRAKVGTPEVNOPTLLYQRYEIKTKMYKGFQALGDAADIRF 60
DB 24 CTCVPPHPOTACNSDLVIRAKVGTPEVNOPTLLYQRYEIKTKMYKGFQALGDAADIRF 83
QY 61 VYTPMESVCGYFHRSHNRSEFLIAGKLODGLIHITTCSPFAPWN 106
DB 84 VYTPMESVCGYFHRSHNRSEFLIAGKLODGLIHITTCSPFAPWN 129
RESULT 4
ID TIM1_BOVIN STANDARD; PRT; 207 AA.
AC P20414; Q9TVB0;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Metalloproteinase inhibitor 1 precursor (TIMP-1) (Embryogenin-1) (EG-
1).
GN TIMP1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RX SEQUENCE FROM N.A.  
RA MEDLINE=90365711; PubMed=2393392;  
RA Preudenstein J., Wagner S., Luck R.M., Einspanier R., Scheit K.H.;  
RT "mRNA of bovine tissue inhibitor of metalloproteinase: sequence and  
RT expression in bovine ovarian tissue";  
RL Biochem. Biophys. Res. Commun. 171:250-256(1990).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=9425757; PubMed=8199264;  
RA Satoh T., Kobayashi K., Yamashita S., Kikuchi M., Sendai Y., Hoshi H.;  
RT "Tissue inhibitor of metalloproteinases (TIMP-1) produced by  
RT granulosa and oviduct cells enhances in vitro development of bovine  
RT embryo";  
RL Biol. Reprod. 50:835-844(1994).  
RN [3]  
RP SEQUENCE OF 25-191 FROM N.A.  
RC TISSUE=Skeletal muscle;  
RA Balcerzak D., Querengesser L., Dixon W.T., Baracos V.E.;  
RT "Involvement of fibroblasts and muscle cells in the expression of an  
RT extracellular proteolytic cascade in bovine skeletal muscle";  
RT Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RN PRELIMINARY SEQUENCE OF 24-69.  
RP MEDLINE=90008914; PubMed=2551903;  
RA de Clerck Y.A., Yean T.D., Ratzkin B.J., Lu H.S., Langley K.E.;  
RT "Purification and characterization of two related but distinct  
RT metalloproteinase inhibitors secreted by bovine aortic endothelial  
RT cells";  
RL J. Biol. Chem. 264:17445-17453(1989).  
CC -!- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)  
CC AND IRREVERSIBLY INACTIVATES THEM.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- PTM: THE ACTIVITY OF TIMP-1 IS DEPENDENT ON THE PRESENCE OF  
CC DISULFIDE BONDS.  
CC -!- SIMILARITY: BELONGS TO THE TIMP FAMILY.  
CC  
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CC  
CC EMBL; M60073; AAA30784.1; -.  
CC EMBL; S70841; AAB30892.1; -.  
CC EMBL; AF144763; AAD30303.1; -.  
CC PIR; A35685; A35685.  
CC PIR; B34468; B34468.  
CC HSSP; P01033; LUFA.  
CC InterPro; IPR001820; TIMP.  
CC Pfam; PF00965; TIMP; 1.  
CC SMART; SM00206; TIMP; 1.  
CC PROSITE; PS00288; TIMP; 1.  
CC Glycoprotein; Metalloprotease inhibitor; Erythrocyte maturation;  
KW Signal.  
FT CHAIN 1 23 METALLOPROTEINASE INHIBITOR 1.  
FT CHAIN 24 207  
FT DISULFID 24 93 BY SIMILARITY.  
FT DISULFID 26 122 BY SIMILARITY.  
FT DISULFID 36 147 BY SIMILARITY.  
FT DISULFID 150 197 BY SIMILARITY.  
FT DISULFID 155 160 BY SIMILARITY.  
FT DISULFID 168 189 BY SIMILARITY.  
FT DISULFID 168 189 N-LINKED (GLCNAC...) (POTENTIAL).  
FT CARBOHYD 53 53 N-LINKED (GLCNAC...) (POTENTIAL).  
FT CARBOHYD 101 101 N-LINKED (GLCNAC...) (POTENTIAL).  
SQ SEQUENCE 207 AA; 23031 MW; E672BEE2B865F3F7 CRC64;  
Query Match 87.7%; Score 508; DB 1; Length 207;

Best Local Similarity 86.8%; Pred. No. 3.7e-51;  
Matches 92; Conservative 6; Mismatches 8; Indels 0; Gaps 0;  
QY 1 CTCVPPHPQTAFNCSDLVIRAKFVGTPTEVNAQTLLYQRYEIKMTKMYKGFQALGDAADIRF 60  
DB 24 CTCVPPHPQTAFNCSDVVIRAKFVGTAENVETALYQRYEIKMTKMYKGFSAIRDAPDIRF 83  
QY 61 VYTPAMESVCGYFRRSHNRSEEFLLIAGKLODGLLHITTCSFVAPWN 106  
DB 84 IYTPAMESVCGYFRRSHNRSEEFLLIAGKLODGLLHITTCSFVAPWN 129  
RESULT 5  
TIMP\_RABIT STANDARD; PRT; 206 AA.  
AC P20614;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Metalloproteinase inhibitor 1 precursor (TIMP-1).  
GN TIMP1.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89214135; PubMed=2708356;  
RA Horowitz S., Dafni N., Shapiro D.L., Holm B.A., Notter R.H.,  
RA Quible D.J.;  
RT "Hyperoxic exposure alters gene expression in the lung. Induction of  
RT the tissue inhibitor of metalloproteinases mRNA and other mRNAs";  
RL J. Biol. Chem. 264:7092-7095(1989).  
CC -!- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)  
CC AND IRREVERSIBLY INACTIVATES THEM.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- PTM: THE ACTIVITY OF TIMP-1 IS DEPENDENT ON THE PRESENCE OF  
CC DISULFIDE BONDS.  
CC -!- SIMILARITY: BELONGS TO THE TIMP FAMILY.  
CC  
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CC  
CC EMBL; J04712; AAA31478.1; -.  
CC PIR; A33350; A33350.  
CC HSSP; P01033; ID2B.  
CC InterPro; IPR001820; TIMP.  
CC Pfam; PF00965; TIMP; 1.  
CC SMART; SM00206; TIMP; 1.  
CC PROSITE; PS00288; TIMP; 1.  
CC Glycoprotein; Metalloprotease inhibitor; Erythrocyte maturation;  
KW Signal.  
FT CHAIN 1 23 METALLOPROTEINASE INHIBITOR 1.  
FT CHAIN 24 206  
FT DISULFID 24 93 BY SIMILARITY.  
FT DISULFID 26 122 BY SIMILARITY.  
FT DISULFID 36 147 BY SIMILARITY.  
FT DISULFID 150 196 BY SIMILARITY.  
FT DISULFID 155 160 BY SIMILARITY.  
FT DISULFID 168 188 BY SIMILARITY.  
FT CARBOHYD 53 53 N-LINKED (GLCNAC...) (POTENTIAL).  
FT CARBOHYD 101 101 N-LINKED (GLCNAC...) (POTENTIAL).  
SQ SEQUENCE 206 AA; 22758 MW; 1839A8DE7174E89E CRC64;  
Query Match 86.6%; Score 507; DB 1; Length 206;  
Best Local Similarity 86.8%; Pred. No. 4.8e-51;  
Matches 92; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

OY 1 CTCVPHPQTAFCSNDLVIRAKFVGTPENVQTLVQRYEIKMTKWKGFQALGDADIRF 60  
 DB 24 CTCVPHPQTAFCSNDLVIRAKFVGAPENVHTTLVQRYEIKMTKWKGFQALGDADIRF 83  
 OY 61 VYTPAMESVCGYFHRSHNRSEFLIAGKLODGLHITTCSPFAPWN 106  
 DB 84 VYTPAMESVCGYFHRSHNRSEFLIAGLQSLHITTCSPFAPWN 129

## RESULT 6

TM1L\_SHEEP STANDARD; PRT; 207 AA.  
 ID TM1L\_SHEEP  
 AC P50122;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Metalloproteinase inhibitor 1 precursor (TIMP-1).  
 GN TIMP1.  
 OS Ovis aries (Sheep).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Caprinae; Ovis.  
 CX NCBI\_TaxID=9940;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Corpus luteum;  
 RX MEDLINE=94102210; PubMed=8275949;  
 RA Smith G.W., Goetz T.L., Anthony R.V., Smith M.F.;  
 RT "Molecular cloning of an ovine ovarian tissue inhibitor of  
 RT metalloproteinases: ontogeny of messenger ribonucleic acid expression  
 RT and in situ localization within preovulatory follicles and luteal  
 RT tissue.";  
 RT Endocrinology 134:344-352 (1994).  
 RL -I- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)  
 CC AND IRREVERSIBLY INACTIVATES THEM.  
 CC -I- SUBCELLULAR LOCATION: Secreted.  
 CC -I- PTM: THE ACTIVITY OF TIMP-1 IS DEPENDENT ON THE PRESENCE OF  
 CC DISULFIDE BONDS.  
 CC -I- SIMILARITY: BELONGS TO THE TIMP FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; S67450; AAB29472.1; -;  
 DR HSSP; P01033; IUEA.  
 DR InterPro; IPR001820; TIMP.  
 DR Pfam; PF00965; TIMP; 1.  
 DR SMART; SM0206; TIMP; 1.  
 DR PROSITE; PS00288; TIMP; 1.  
 KW Glycoprotein; Metalloproteinase inhibitor; Erythrocyte maturation;  
 KW Signal.  
 FT SIGNAL 1 23 BY SIMILARITY.  
 FT CHAIN 24 207 METALLOPROTEINASE INHIBITOR 1.  
 FT DISULFID 24 93 BY SIMILARITY.  
 FT DISULFID 26 122 BY SIMILARITY.  
 FT DISULFID 36 147 BY SIMILARITY.  
 FT DISULFID 150 197 BY SIMILARITY.  
 FT DISULFID 155 160 BY SIMILARITY.  
 FT DISULFID 168 189 BY SIMILARITY.  
 FT CARBOHYD 53 53 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT CARBOHYD 101 101 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SEQUENCE 207 AA; 23057 MW; 1D3BCA2012F80E46 CRC64;

Query Match 87.0%; Score 504; DB 1; Length 207;  
 Best local Similarity 85.8%; Pred. No. 1,1e-50;  
 Matches 91; Conservative 7; Mismatches 8; Indels 0; Gaps 0;  
 OY 1 CTCVPHPQTAFCSNDLVIRAKFVGTPENVQTLVQRYEIKMTKWKGFQALGDADIRF 60

DB 24 CTCVPHPQTAFCSNDLVIRAKFVGTAENETALVQRYEIKMTKWKGFQALGDADIRF 83  
 OY 61 VYTPAMESVCGYFHRSHNRSEFLIAGKLODGLHITTCSPFAPWN 106  
 DB 84 VYTPAMESVCGYFHRSHNRSEFLIAGLQSLHITTCSPFAPWN 129

## RESULT 7

TM1L\_PIG STANDARD; PRT; 207 AA.  
 ID TM1L\_PIG  
 AC P35624; Q9TT83; Q9TTB9;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Metalloproteinase inhibitor 1 precursor (TIMP-1).  
 GN TIMP1.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 CX NCBI\_TaxID=99823;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Ovary;  
 RX MEDLINE=92201478; PubMed=1312961;  
 RA Tanaka T., Andon N., Takeya T., Sato E.;  
 RT "Differential screening of ovarian cDNA libraries detected the  
 RT expression of the porcine collagenase inhibitor gene in functional  
 RT corpora lutea.";  
 RT Mol. Cell. Endocrinol. 83:65-71 (1992).  
 RN (2)  
 RP SEQUENCE OF 34-195 FROM N.A.  
 RA Wang J.Y., Baer A.E., Kraus V.B., Setton L.A.;  
 RT "Gene expression level of mmp3 and timp1 in interveterbral disc.";  
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
 RN (3)  
 RP SEQUENCE OF 37-144 FROM N.A.  
 RC TISSUE=Skin;  
 RA Wang J.F., Boykiv R.H., Reno C.R., Hart D.A., Olson M.E.;  
 RT "Cloning and sequencing of porcine TIMP-1.";  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 CC -I- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)  
 CC AND IRREVERSIBLY INACTIVATES THEM.  
 CC -I- SUBCELLULAR LOCATION: Secreted.  
 CC -I- PTM: THE ACTIVITY OF TIMP-1 IS DEPENDENT ON THE PRESENCE OF  
 CC DISULFIDE BONDS.  
 CC -I- SIMILARITY: BELONGS TO THE TIMP FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; S96211; AAB21865.1; -;  
 DR EMBL; AF201726; AAF24348.1; -;  
 DR EMBL; AF156029; AAF17354.1; -;  
 DR HSSP; P01033; IUEA.  
 DR InterPro; IPR001820; TIMP.  
 DR Pfam; PF00965; TIMP; 1.  
 DR SMART; SM0206; TIMP; 1.  
 DR PROSITE; PS00288; TIMP; 1.  
 KW Glycoprotein; Metalloproteinase inhibitor; Erythrocyte maturation;  
 KW Signal.  
 FT SIGNAL 1 23 BY SIMILARITY.  
 FT CHAIN 24 207 METALLOPROTEINASE INHIBITOR 1.  
 FT DISULFID 24 93 BY SIMILARITY.  
 FT DISULFID 26 122 BY SIMILARITY.  
 FT DISULFID 36 147 BY SIMILARITY.  
 FT DISULFID 150 197 BY SIMILARITY.  
 FT DISULFID 155 160 BY SIMILARITY.

Query Match 87.0%; Score 504; DB 1; Length 207;  
 Best local Similarity 85.8%; Pred. No. 1,1e-50;  
 Matches 91; Conservative 7; Mismatches 8; Indels 0; Gaps 0;  
 OY 1 CTCVPHPQTAFCSNDLVIRAKFVGTPENVQTLVQRYEIKMTKWKGFQALGDADIRF 60

FT	DISULFID	150	197	BY SIMILARITY.
FT	DISULFID	155	160	BY SIMILARITY.
FT	DISULFID	168	189	BY SIMILARITY.
FT	CARBOHYD	53	53	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	101	101	N-LINKED (GLCNAC. . .) (POTENTIAL)
SEQ	SEQUENCE	207 AA;	23046 MW;	FD710DA98D168070 CRC64;

Query Match 82.4%; Score 477; DB 1; Length 207;  
 Best Local Similarity 83.0%; Pred. No. 1.3e-47;  
 Matches 88; Conservative 7; Mismatches 11; Indels 0; Gaps

QY	1	CTCVPHPQTACNSDLVIRAKFVGTSEVNVQTTLYQRYEIKMTKMKVGFQALGDAADIRF	60
DB	24	CTCVPHPQTACFSEFVIRAKFVGTSEVNVQTTLQRRYEIKMTKMPGFSALGDAPDTWF	83
QY	61	VYTPAMESVCGYFHRSHNRSEFLIAGKLODGLLHITTCFSFVAPWN	106
DB	84	VYTPAMESLCGYFHRSENRSEFLIAGQLLDEKLYITTCFSFVAPWN	129

RESULT 9  
 TIM1 MOUSE  
 ID TIM1 MOUSE STANDARD; PRT; 205 AA.  
 AC F12032; P20064;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Metalloproteinase inhibitor 1 precursor (TIMP-1) (Brythroid  
 DE potentiating activity) (EPA) (Tissue inhibitor of metalloproteinases  
 DE (Collagenase inhibitor 16C8 fibroblast) (TPA-induced protein)  
 DE (TPA-SI).  
 DE TIMP1 OR TIMP-1 OR TIMP.  
 GN Mus musculus (Mouse).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_Taxid=10090;  
 RN [1]  
 RN MEDLINE=87218524; PubMed=3034603;  
 RP Gewert D.R., Coulombe B., Castellino M., Skup D., Williams B.R.G.;  
 RA "Characterization and expression of a murine gene homologous to huma  
 RT EPA/TIMP: a virus-induced gene in the mouse.";  
 RL EMBO J. 6:651-657(1987).  
 RN [2]  
 RN MEDLINE=87066763; PubMed=3024122;  
 RP Edwards D.R., Waterhouse P., Holman M.L., Denhardt D.T.;  
 RA "A growth-responsive gene (16C8) in normal mouse fibroblasts  
 RT homologous to a human collagenase inhibitor with  
 RT erythroid-potentiating activity: evidence for inducible and  
 RT constitutive transcripts".  
 RL Nucleic Acids Res. 14:8863-8878(1986).  
 RN [3]  
 RN MEDLINE=88038821; PubMed=3670294;  
 RP Johnson M.B., Housey G.M., Kirschmeier P.T., Weinstein I.B.;  
 RA "Molecular cloning of gene sequences regulated by tumor promoters an  
 RT mitogens through protein kinase C.";  
 RL Mol. Cell. Biol. 7:2821-2829(1987).  
 CC -1- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES  
 CC AND IRREVERSIBLY INACTIVATES THEM. ALSO MEDIATES ERYTHROPOIESIS  
 CC VITRO, BUT, UNLIKE IL-3, IT IS SPECIES-SPECIFIC, STIMULATING THE  
 CC GROWTH AND DIFFERENTIATION OF ONLY HUMAN AND MURINE ERYTHROID  
 CC PROGENITORS.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: FOUND IN FETAL AND ADULT TISSUES. HIGHEST  
 CC LEVELS ARE FOUND IN BONE. ALSO FOUND IN LUNG, OVARY AND UTERUS.  
 CC -1- INDUCTION: REGULATED BY TUMOR PROMOTERS AND MITOGENS THROUGH  
 CC PROTEIN KINASE C. ALSO INDUCED BY VIRUSES.  
 CC -1- PTM: THE ACTIVITY OF TIMP-1 IS DEPENDENT ON THE PRESENCE OF  
 CC DISULFIDE BONDS.

Query Match	Best local	Similarity	Score	DB 1:	Length	207:			
Matches	83:	Conservative	9:	Mismatches	14:	Indels	0:	Gaps	0:
Qy	1	CTCVPHPHQAFCNSDLVIRAKFVGTGEVNVQTTLYQRYEIKMTMYKGFQALGDAADIRF	60						
Db	24	CTCAAPHQGTALCNSQIVIRAKFVGTGAEVNVQTTDLNRRYEIKMTGTFPGFSLGNASDIRF	83						
Qy	61	VYTPAMBSVCGYFPRSHNRSEEPILAGLQDGLLHITTCGFVAEWN	106						

Db 84 VDTPALESVCGYLRHSQRSEEFVLVAGNLRDGHLQINTCSFVAPWS 129

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RESULT 11
TIM1_RAT
ID TIM1_RAT STANDARD; PRT; 217 AA.
AC P30120; P70533;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Metalloprotease inhibitor 1 precursor (TIMP-1).
GN TIMP1 OR TIMP-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Skin dorsal;
RA MEDLINE=95011636; PubMed=7926820;
RA Okada A., Garnier J.M., Vicaire S., Bassett P.;
RT "Cloning of the cDNA encoding rat tissue inhibitor of
RT metalloprotease 1 (TIMP-1), amino acid comparison with other TIMPs,
RT and gene expression in rat tissues.";
RL Gene 147:301-302(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Gibbons K.L., O'Grady R.L., Piper A.A.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 30-205 FROM N.A.
RC TISSUE=Liver;
RA Iredale J.P., Benyon R.C., Arthur M.J.P., Ferris W.F., Alcolado R.,
RA Winwood P.J., Clark N., Murphy G.;
RT "Tissue inhibitor of metalloprotease-1 messenger RNA expression is
RT enhanced relative to interstitial collagenase messenger RNA in
RT experimental liver injury and fibrosis.";
RL Hepatology 24:176-184(1996).
RN [4]
RP SEQUENCE OF 19-156 FROM N.A., SEQUENCE OF 24-38, INDUCTION, FUNCTION,
RP AND SUBCELLULAR LOCATION.
RC STRAIN=Sprague-Dawley; TISSUE=Sertoli cells;
RX MEDLINE=95296691; PubMed=777858;
RA Boujrad N., Ogwegbu S.O., Garnier M., Lee C.-H., Martin B.M.,
RA Papadopoulos V.;
RT "Identification of a stimulator of steroid hormone synthesis isolated
RT from testis.";
RL Science 268:1609-1612(1995).
RN [5]
RP SEQUENCE OF 24-45.
RX MEDLINE=92117648; PubMed=1309971;
RA Roswit W.T., McCourt D.W., Partridge N.C., Jeffrey J.J.;
RT "Purification and sequence analysis of two rat tissue inhibitors of
RT metalloproteases.";
RL Arch. Biochem. Biophys. 292:402-410(1992).
CC -!- FUNCTION: Complexes with metalloproteases (such as collagenases)
CC and irreversibly inactivates them. Also stimulates steroidogenesis
CC by Leydig and ovarian granulosa cells; procathepsin L is required
CC for maximal activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- INDUCTION: By follicle-stimulating hormone (FSH).
CC -!- PTM: THE ACTIVITY OF TIMP-1 IS DEPENDENT ON THE PRESENCE OF
CC DISULFIDE BONDS.
CC -!- SIMILARITY: BELONGS TO THE TIMP FAMILY.
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CC EMBL; U06179; AAA85780.1; -
CC EMBL; L31883; AAA85373.1; -
CC EMBL; L29512; AAB08483.1; -
CC EMBL; U16022; AAA51653.1; ALT_SEQ.
CC PIR; S20326; S20326.
CC HSP; P01033; IUEA.
CC InterPro; IPR001820; TIMP.
CC Pfam; PF00965; TIMP; 1.
CC SMART; SM00206; TIMP; 1.
CC PROSITE; PS00288; TIMP; 1.
CC Glycoprotein; Metalloprotease inhibitor; Erythrocyte maturation;
KW Steroidogenesis; Signal.
FT SIGNAL 1 23
FT CHAIN 24 217 METALLOPROTEINASE INHIBITOR 1.
FT DISULFID 24 93 BY SIMILARITY.
FT DISULFID 26 122 BY SIMILARITY.
FT DISULFID 36 147 BY SIMILARITY.
FT DISULFID 150 197 BY SIMILARITY.
FT DISULFID 155 160 BY SIMILARITY.
FT DISULFID 168 189 BY SIMILARITY.
FT CARBOHYD 77 77 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 101 101 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 80 81 GF -> DI (IN REF. 3).
FT CONFLICT 88 88 A -> V (IN REF. 4).
FT CONFLICT 103 103 S -> R (IN REF. 3).
FT CONFLICT 129 130 HN -> AS (IN REF. 3).
FT CONFLICT 136 140 OKAFV -> RKGLT (IN REF. 3).
FT CONFLICT 149 149 V -> L (IN REF. 4).
FT CONFLICT 157 157 A -> V (IN REF. 3).
FT CONFLICT 166 166 S -> T (IN REF. 3).
FT CONFLICT 185 187 DHF -> RHL (IN REF. 3).
FT CONFLICT 195 195 D -> G (IN REF. 3).
FT CONFLICT 201 201 Y -> S (IN REF. 3).
FT CONFLICT 204 205 VS -> SR (IN REF. 3).
SQ SEQUENCE 217 AA; 23793 MW; C5AC240A61C1A1DF CRC64;
Query Match 77.0%; Score 446; DB 1; Length 217;
Best Local Similarity 73.6%; Pred. No. 5.2e-44;
Matches 78; Conservative 14; Mismatches 14; Indels 0; Gaps 0;
Oy 1 CTCVPPHQTAFCSNLDVIRAKFVGTPEVNTQTLVQRYEIKMTMYKGFQALGDAADIRF 60
Db 24 CSCAPHTPQTAFCSNLDVIRAKFMGSPETITLYQRYEIKMTMYKGFQALGDAADIRF 83
Oy 61 VYTPAMESVCCGYFHRSHNRSEEFLLAGLQDGLLHITTCSPVAPWN 106
Db 84 AYTPAMESLCGYVHKHSQRSEEFLLAGLQDGLLHITTCSPVAPWN 129
RESULT 12
TIM3_SCYTO
ID TIM3_SCYTO STANDARD; PRT; 214 AA.
AC Q9W6B4;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Metalloprotease inhibitor 3 precursor (TIMP-3) (Tissue inhibitor of
DE metalloproteases-3).
GN TIMP3.
OS Scyliorhinus torazame (Cloudy catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC Scyliorhinidae; Scyliorhinus.
OX NCBI_TaxID=75743;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cartilage;
RX PubMed=11342115;
RA Kim J.T., Kim M.-S., Bae M.-K., Ahn M.-Y., Kim Y.-J.,
RA Lee S.-J., Kim K.-W.;
RT "Cloning and characterization of tissue inhibitor of
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RT metalloproteinase-3 (TIMP-3) from shark, Scyliorhinus torazame." ;
RL Biochim. Biophys. Acta 1517:311-315(2001).
CC -!- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
CC AND IRREVERSIBLY INACTIVATES THEM. MAY FORM PART OF A TISSUE-
CC SPECIFIC ACUTE RESPONSE TO REMODELING STIMULI (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted. Extracellular matrix (By
CC similarity).
CC -!- TISSUE SPECIFICITY: Expressed abundantly in brain and cartilage.
CC -!- SIMILARITY: BELONGS TO THE TIMP FAMILY.
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P D EMBL, AF110767; AAD26150.1; -.
P HSSP, P16035; 2TMP.
DR InterPro: IPR001820; TIMP.
DR Pfam: PF00965; TIMP; 1.
DR SMART, SM00206; TIMP; 1.
DR PROSITE, PS00288; TIMP; 1.
KW Metalloprotease inhibitor; Signal.
FT SIGNAL 1 26
FT CHAIN 1 26 METALLOPROTEINASE INHIBITOR 3.
FT DISULFID 27 214
FT DISULFID 27 94 BY SIMILARITY.
FT DISULFID 29 121 BY SIMILARITY.
FT DISULFID 39 146 BY SIMILARITY.
FT DISULFID 148 195 BY SIMILARITY.
FT DISULFID 153 158 BY SIMILARITY.
FT DISULFID 166 187 BY SIMILARITY.
FT CARBOHYD 210 210 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 214 AA; 2499 MW; BCAD300B8E483557 CRC64;

Query Match 40.6%; Score 235; DB 1; Length 214;
Best Local Similarity 43.0%; Pred. No. 9.2e-20;
Matches 46; Conservative 19; Mismatches 36; Indels 6; Gaps 3;

OY 1 CTCVPHPQTACNSDLVIRAKFVGTPEVNOQTL-YORYEIKTKMYKGFQALGDAADIR 59
DB 27 CTCMGNHPQEARCNSDIVIRAKVKGKLLKDGPGFTMRITIKOMKMYRGFSKM---QQVQ 83
OY 60 FVYTPAMESVCGYFHRSHRSEFLIAGLQDGLHITTCSPVAPWN 106
DB 84 YIYTRAEBSLGCY--RLQYNKFQYLITGRVFDGEVYTVGVCFIVPWD 128

RESULT 13
TIM2_HUMAN STANDARD; PRT; 220 AA.
AC Q9WOC6;
DT 16-OCT-2001 (Rel. 40; Created)
DT 16-OCT-2001 (Rel. 40; Last sequence update)
DT 16-OCT-2001 (Rel. 40; Last annotation update)
DE Metalloproteinase inhibitor 2 precursor (TIMP-2) (Tissue inhibitor of
DE metalloproteinases-2).
GN TIMP2.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognath; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Hartley; TISSUE=Lung;
RX MEDLINE=20215260; PubMed=10749751;
RA Melendez J., Maldonado V., Selman M., Pardo A.;
RT "Cloning and expression of guinea pig TIMP-2. Expression in normal and
RT hyperoxic lung injury."
RL Am. J. Physiol. 278:1737-L743(2000).
CC -!- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
CC AND IRREVERSIBLY INACTIVATES THEM.
```

```
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN THE LUNG IN
CC ALVEOLAR MACROPHAGES AND EPITHELIAL CELLS. ALSO FOUND IN BRAIN,
CC KIDNEY, INTESTINE, SPLEEN, AND HEART.
CC -!- PTM: THE ACTIVITY OF TIMP-2 IS DEPENDENT ON THE PRESENCE OF
CC DISULFIDE BONDS.
CC -!- SIMILARITY: BELONGS TO THE TIMP FAMILY.
-----
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CC or send an email to license@ibb-sib.ch).
-----
P D EMBL, AF127803; AAD28252.1; -.
P HSSP, P16035; 1BR9.
DR InterPro: IPR001820; TIMP.
DR Pfam: PF00965; TIMP; 1.
DR SMART, SM00206; TIMP; 1.
DR PROSITE, PS00288; TIMP; 1.
KW Metalloprotease inhibitor; Signal.
FT SIGNAL 1 26
FT CHAIN 1 220 METALLOPROTEINASE INHIBITOR 2.
FT DISULFID 27 98 BY SIMILARITY.
FT DISULFID 29 127 BY SIMILARITY.
FT DISULFID 39 152 BY SIMILARITY.
FT DISULFID 154 201 BY SIMILARITY.
FT DISULFID 159 164 BY SIMILARITY.
FT DISULFID 172 193 BY SIMILARITY.
SQ SEQUENCE 220 AA; 24318 MW; 2A2541764755B9AF CRC64;

Query Match 40.4%; Score 234; DB 1; Length 220;
Best Local Similarity 44.7%; Pred. No. 1.2e-19;
Matches 51; Conservative 15; Mismatches 34; Indels 14; Gaps 5;

OY 1 CTCVPHPQTACNSDLVIRAKFVGTPEVNO-TTLYO-----RYEIKTKMYKGFQALG 53
DB 27 CSCSPVHPQAFNCADVVIRAKAVSEKEDVSGNDIYGNPIRKIORYEIKQIKMFK-----G 81
OY 54 DADIRFVYTPAMESVCGYFHRSHRSEFLIAGLQ-DGLHITTCSPVAPWN 106
DB 82 PKKDIEFYITASAVCG-VSLDVGKKEKYLIAKAEQDGMHITLCDFIVPWD 134

RESULT 14
TIM2_HUMAN STANDARD; PRT; 220 AA.
AC P16035; Q93006; Q16121; Q9UDF7;
DT 01-APR-1990 (Rel. 14; Created)
DT 01-NOV-1990 (Rel. 16; Last sequence update)
DT 16-OCT-2001 (Rel. 40; Last annotation update)
DE Metalloproteinase inhibitor 2 precursor (TIMP-2) (Tissue inhibitor of
DE metalloproteinases-2) (CSC-21K).
GN TIMP2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=90338014; PubMed=2380196;
RA Stetler-Stevenson W.G., Brown P.D., Onisto M., Levy A.T., Liotta L.A.;
RT "Tissue inhibitor of metalloproteinases-2 (TIMP-2) mRNA expression in
RT tumor cell lines and human tumor tissues."
RL J. Biol. Chem. 265:13933-13938(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE=90207285; PubMed=2157214;
RA Boone T.C., Johnson M.J., de Clerck Y.A., Langley K.E.;
RT "cDNA cloning and expression of a metalloproteinase inhibitor related
RT to tissue inhibitor of metalloproteinases." ;
```





Db 82 PEKDIFFIYTA PSSAVCG-VSLDVGSGKEYLLIAGKAGDGKWHITLCDPIVPMW 134

## RESULT 15

TIM2\_CRIL0 STANDARD; PRT; 196 AA.  
 AC Q60453;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Metalloproteinase inhibitor 2 precursor (TIMP-2) (Tissue inhibitor of  
 DE metalloproteinases-2) (Fragment).  
 GN TIMP2.  
 OS Cricetus longicaudatus (long-tailed hamster) (Chinese hamster).  
 OC Eukaryota; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Cricetus  
 CC NCBI\_TaxId=10030;  
 CC (1)  
 CC SEQUENCE FROM N.A.  
 CC TISSUE=Ovary;  
 RA Suzuki Y.;  
 RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.  
 CC -! FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)  
 CC AND IRREVERSIBLY INACTIVATES THEM (BY SIMILARITY).  
 CC -! SUBCELLULAR LOCATION: Secreted.  
 CC -! PTM: THE ACTIVITY OF TIMP-2 IS DEPENDENT ON THE PRESENCE OF  
 CC DISULFIDE BONDS (BY SIMILARITY).  
 CC -! SIMILARITY: BELONGS TO THE TIMP FAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: X75924; CAA53528.1; -  
 CC HSSP: P16035; 1BR9.  
 DR InterPro: IPR001820; TIMP.  
 DR Pfam: PF00965; TIMP; 1.  
 DR SMART: SM00206; TIMP; 1.  
 DR PROSITE: PS00288; TIMP; 1.  
 KW Metalloprotease inhibitor; Signal.  
 FT NON\_TER 1  
 FT SIGNAL 1  
 FT CHAIN 2  
 FT DISULFID 3 196 BY SIMILARITY.  
 FT DISULFID 3 196 METALLOPROTEINASE INHIBITOR 2.  
 FT DISULFID 5 103 BY SIMILARITY.  
 FT DISULFID 15 128 BY SIMILARITY.  
 FT DISULFID 130 177 BY SIMILARITY.  
 FT DISULFID 135 140 BY SIMILARITY.  
 FT DISULFID 148 169 BY SIMILARITY.  
 SQ SEQUENCE 196 AA; 21941 MW; 2ADAB9B54AF75381 CRC64;  
 Query Match 40.2%; Score 233; DB 1; Length 196;  
 Best Local Similarity 44.7%; Pred. No. 14e-19;  
 Matches 51; Conservative 15; Mismatches 34; Indels 14; Gaps 5;  
 QY 1 CTCVPPHPQTAFCSNLDVIRAKFVGTPENVQ--TLYQ-----RYEIKMTKMYKGFQALG 53  
 Db 3 CSCSPVHPQOARNDVIRAKAVSEKVDSDNDIGNIKRIQYIKQIKMKF-----G 57  
 QY 54 DAADIRFVYTPPMESVCGYFHRSHNRSEFLIAGKIQ-DGLIHITTCGTFVAPWN 106  
 Db 58 PKDIEFIYTA PSSAVCG-VSLDVGSGKEYLLIAGKAGDGKWHITLCDPIVPMW 110

Search completed: December 17, 2002, 15:04:52  
 Job time : 5.84828 secs

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ID Q9MZ12 PRELIMINARY; PRT; 137 AA.
AC Q9MZ12;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Tissue inhibitor of metalloproteinase 1 (Fragment).
GN TIMP1.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20347710; PubMed=10898873;
RA Galloway S.M., McNatty K.P., Cambridge L.M., Laitinen M.P.E.,
RA Juengel J.L., Jokiranta S., McLaren R.J., Luiro K., Dodds K.D.,
RA Montgomery G.W., Beattie A.E., Davis G.H., Ritvos O.;
RT "Mutations in an oocyte-derived growth factor (BMP15) cause increased
RT ovulation rate and infertility in a dosage-sensitive manner.";
RL Nat. Genet. 25:279-283(2000).
DR EMBL; AF268477; AAF81746.1; -.
DR HSSP; P01033; 102B.
DR InterPro; IPR001820; TIMP.
DR Pfam; PF00965; TIMP; 1.
DR SMART; SM00206; TIMP; 1.
FT NON_TER 1
FT NON_TER 137
SQ SEQUENCE 137 AA; 15396 MW; 62009B069D0594B7 CRC64;

Query Match 80.0%; Score 463; DB 6; Length 137;
Best Local Similarity 85.0%; Pred. No. 4.5e-46;
Matches 85; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 7 HPQAFNCNSDLVIRAKFVGTPEVNOTLYQRYEIKWTMYKGFQALGDAAADIRFVYTPAM 66
Db 1 HPQAFNCNSDLVIRAKFVGTAEVNTALYQRYEIKWTMYKGFQALGDAAADIRFVYTPAM 60
Qy 67 ESVCGYFHRSHNRSEEFILAGKLOGLLHITTCSFVAPWN 106
Db 61 ESVCGYFHRSHNRSEEFILAGKLOGLLHITTCSFVAPWN 100

RESULT 3
Q925Q6 PRELIMINARY; PRT; 194 AA.
ID Q925Q6;
AC Q925Q6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Tissue inhibitor of matrix metalloproteinase-2 (Fragment).
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RX KO K.H., Shin C.Y., Lee W.J., Yoo B.K., Ryu J.R., Park K.H.;
RT "Expression of metalloproteinase-2 (gelatinase A) and tissue inhibitor
RT of metalloproteinase-2 (TIMP-2) from hamster tracheal goblet cells: a
RT possible role in upper airway inflammation.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF260255; AAK51636.1; -.
DR InterPro; IPR001820; TIMP.
DR Pfam; PF00965; TIMP; 1.
FT NON_TER 1
FT NON_TER 194
SQ SEQUENCE 194 AA; 21763 MW; 1C5D10A3038A8941 CRC64;

Query Match 38.3%; Score 222; DB 11; Length 194;
Best Local Similarity 43.0%; Pred. No. 7.8e-18;
Matches 49; Conservative 16; Mismatches 35; Indels 14; Gaps 5;
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Qy 1 CTCVPPHPOTAFNCNSDLVIRAKFVGTPEVNOQ-TTLYQ-----RYEIKWTMYKGFQALG 53
Db 1 CSCSPVHQQAFCNADVVIRAKVSEKVDGNDIYGNPVKRIQYKIRKMFK-----G 55
Qy 54 DAAADIRFVYTPAMESVCGYFHRSHNRSEEFILAGKLO-DGLLHITTCSFVAPWN 106
Db 56 PKDIEFIYAPSSAMCG-VSLDVGKGKEYLIAGKAGDGKMHITLCDFIIVPND 108

RESULT 4
Q91ZP7 PRELIMINARY; PRT; 145 AA.
ID Q91ZP7;
AC Q91ZP7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Tissue inhibitor of metalloproteinase 1 (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=WISTAR; TISSUE-OVARY;
RA Espey L.L., Ujioka T., Okamura H., Richards J.S.;
RT "Expression of metallothionein-1 (MT-1) in steroid-secreting cells of
RT the rat ovary during the peri-ovulatory period following gonadotropin
RT treatment.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF411319; AAL05862.1; -.
DR InterPro; IPR001820; TIMP.
DR Pfam; PF00965; TIMP; 1.
FT NON_TER 1
FT NON_TER 145
SQ SEQUENCE 145 AA; 15954 MW; 7EC7053DA82DE913 CRC64;

Query Match 37.8%; Score 219; DB 11; Length 145;
Best Local Similarity 67.9%; Pred. No. 1.2e-17;
Matches 38; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

Qy 51 ALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFILAGKLOGLLHITTCSFVAPWN 106
Db 2 AVGNATGFRFAYTPAMESLCGYVHKSQNRSEEFILAGLRNGLHITACSLVLPWH 57

RESULT 5
Q95KL7 PRELIMINARY; PRT; 126 AA.
ID Q95KL7;
AC Q95KL7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Tissue inhibitor of matrix metalloproteinase-3 (Fragment).
GN TIMP-3.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX Ji S., Wang Y., Li H., Ji W., Piao Y.;
RT "Cloning and characterization of tissue inhibitor of matrix
RT metalloproteinase-3 (TIMP-3) cDNA from Macaca mulatta.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF366399; AAK53706.1; -.
DR InterPro; IPR001820; TIMP.
DR Pfam; PF00965; TIMP; 1.
FT NON_TER 1
FT NON_TER 126
SQ SEQUENCE 126 AA; 14690 MW; 2F162249A7D2615E CRC64;
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Query Match 28.5%; Score 165; DB 6; Length 126;  
 Best Local Similarity 37.8%; Pred. No. 2e-11;  
 Matches 37; Conservative 20; Mismatches 31; Indels 10; Gaps 4;

OY 12 FNSDLVIRAKVGVPEVNO---TTLQRYEIKMTKMYGFOALGDAADIRFYTPAMES 68  
 DB 1 FNSDLVIRAKVGVKLVGEGFTLV--YTIKMKMYRGFTKM--PHVOYIHTSEAS 55

OY 69 VCGFYHSHNRSEEFLLAGKLDGLHITTCSPVAPWN 106  
 DB 56 LCGL--KLEVNKYQYLLTGRVYDGKMYTGLCNFVERWD 91

RESULT 6  
 OYTB7 PRELIMINARY; PRT; 152 AA.

ID O9TB7  
 AC O9TB7; 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE Metalloproteinase inhibitor 3 (TIMP-3) (Tissue inhibitor of metalloproteinases-3) (Fragment).  
 GN TIMP-3.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OC NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Wang J.F., Boykiw R.H., Reno C.R., Hart D.A., Olson M.E.;  
 RT "Cloning and sequencing of porcine TIMPs."  
 RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.  
 CC - FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES) AND IRREVERSIBLY INACTIVATES THEM. MAY FORM PART OF A TISSUE-SPECIFIC ACUTE RESPONSE TO REMODELING STIMULI.  
 CC - SUBCELLULAR LOCATION: EXTRACELLULAR.  
 CC - SIMILARITY: BELONGS TO THE TIMP FAMILY.  
 DR EMBL; AF156031; AAF17356.1; --  
 DR HSSP; P16035; 1BR9.  
 DR InterPro; IPR001820; TIMP.  
 DR Pfam; PF00965; TIMP; 1.  
 DR SMART; SMO0206; TIMP; 1.  
 DR Metalloproteinase inhibitor.  
 FT NON\_TER 1 1  
 FT DISULFID 2 109 BY SIMILARITY.  
 FT DISULFID 116 121 BY SIMILARITY.  
 FT DISULFID 129 150 BY SIMILARITY.  
 FT NON\_TER 152 152  
 GN SEQUENCE 152 AA; 1736 MW; 40505F5FCS8B5E7 CRC64;

Query Match 27.5%; Score 159; DB 6; Length 152;  
 Best Local Similarity 37.1%; Pred. No. 1.3e-10;  
 Matches 36; Conservative 20; Mismatches 31; Indels 10; Gaps 4;

OY 13 CNSDLVIRAKVGVPEVNO---TTLQRYEIKMTKMYGFOALGDAADIRFYTPAMES 69  
 DB 2 CNSDLVIRAKVGVKLVGEGFTLV--YTIKMKMYRGFTKM--PHVOYIHTSEAS 56

OY 70 CGFYHSHNRSEEFLLAGKLDGLHITTCSPVAPWN 106  
 DB 57 CGL--KLEVNKYQYLLTGRVYDGKMYTGLCNFVERWD 91

RESULT 7  
 OYTB8 PRELIMINARY; PRT; 138 AA.

ID O9TB8  
 AC O9TB8; 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE Metalloproteinase inhibitor 2 (TIMP-2) (Tissue inhibitor of metalloproteinases-2) (Fragment).  
 GN TIMP-2.

OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OC NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Wang J.F., Boykiw R.H., Reno C.R., Hart D.A., Olson M.E.;  
 RT "Cloning and sequencing of porcine TIMPs."  
 RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.  
 CC - FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES) AND IRREVERSIBLY INACTIVATES THEM.  
 CC - SUBCELLULAR LOCATION: EXTRACELLULAR.  
 CC - SIMILARITY: BELONGS TO THE TIMP FAMILY.  
 DR EMBL; AF156030; AAF17355.1; --  
 DR HSSP; P16035; 1BR9.  
 DR InterPro; IPR001820; TIMP.  
 DR Pfam; PF00965; TIMP; 1.  
 DR SMART; SMO0206; TIMP; 1.  
 DR Metalloproteinase inhibitor.  
 FT NON\_TER 1 1  
 FT DISULFID 117 122 BY SIMILARITY.  
 FT NON\_TER 138 138  
 GN SEQUENCE 138 AA; 15596 MW; F43F13651F45C348 CRC64;

Query Match 26.4%; Score 153; DB 6; Length 138;  
 Best Local Similarity 39.8%; Pred. No. 5.6e-10;  
 Matches 39; Conservative 13; Mismatches 32; Indels 14; Gaps 5;

OY 17 LVIRAKVGVPEVNO---TTLQRYEIKMTKMYGFOALGDAADIRFYTPAMES 69  
 DB 1 LVIRAKVGVKLVGEGFTLV--YTIKMKMYRGFTKM--PHVOYIHTSEAS 55

OY 70 CGFYHSHNRSEEFLLAGKLDGLHITTCSPVAPWN 106  
 DB 56 CG--VSLDIGKKVYLLAGKAGHGHITLCPFVPWD 92

RESULT 8  
 OYTB6 PRELIMINARY; PRT; 170 AA.

ID O9TB6  
 AC O9TB6; 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Metalloproteinase inhibitor 4 (TIMP-4) (Tissue inhibitor of metalloproteinases-4) (Fragment).  
 GN TIMP-4.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OC NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Wang J.F., Boykiw R.H., Reno C.R., Hart D.A., Olson M.E.;  
 RT "Cloning and sequencing of porcine TIMPs."  
 RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.  
 CC - FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES) AND IRREVERSIBLY INACTIVATES THEM.  
 CC - SUBCELLULAR LOCATION: EXTRACELLULAR.  
 CC - SIMILARITY: BELONGS TO THE TIMP FAMILY.  
 DR EMBL; AF156032; AAF17357.1; --  
 DR HSSP; P16035; 2TMP.  
 DR InterPro; IPR001820; TIMP.  
 DR Pfam; PF00965; TIMP; 1.  
 DR SMART; SMO0206; TIMP; 1.  
 DR Metalloproteinase inhibitor.  
 FT NON\_TER 1 1  
 FT DISULFID 107 154 BY SIMILARITY.  
 FT DISULFID 112 117 BY SIMILARITY.  
 FT DISULFID 125 146 BY SIMILARITY.  
 FT NON\_TER 170 170

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DR HSSP: P01033; LUEA.
DR InterPro: IPR001820; TIMP.
DR Pfam: PF00965; TIMP; 1.
DR PROSITE: PS00288; TIMP; 1.
DR SEQUENCE 25 AA; 2698 MW; 35129B2B74C1FDAF CRC64;

Query Match: 21.4%; Score 124; DB 11; Length 25;
Best Local Similarity 84.0%; Pred. NO. 1.8e-07;
Matches 21; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTCVPPHPQTAFCNSDLVIRAKFVG 25
DB 1 CSCAPTHPQTAFCNSDLVIRAKFMG 25

RESULT 11
O9QV13 PRELIMINARY; PRT; 25 AA.
AC O9QV13;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
DE Collagenase inhibitor MS-31 (Fragment).
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10095;
RN [1]
RP SEQUENCE
RX MEDLINE=95105266; PubMed=7806596;
RA Rosenthal R.A., Moses M.A., Shintani Y., Megyesi J.F., Langer R.,
RT "Purification and characterization of two collagenase inhibitors from
RT mouse sarcoma 180 conditioned medium.";
RL J. Cell. Biochem. 56:97-105(1994).
DR HSSP: P01033; LUEA.
DR InterPro: IPR001820; TIMP.
DR Pfam: PF00965; TIMP; 1.
DR SEQUENCE 25 AA; 2678 MW; 923226E82C1901FD CRC64;

Query Match: 21.4%; Score 124; DB 11; Length 25;
Best Local Similarity 84.0%; Pred. NO. 1.8e-07;
Matches 21; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 TCVPPHPQTAFCNSDLVIRAKFVGT 26
DB 1 SCAPHPQTAFCNSDLVIRAKFMGS 25

RESULT 12
O9GPJ2 PRELIMINARY; PRT; 221 AA.
AC O9GPJ2;
DT 01-MAR-2001 (TEMBLrel. 16, Created)
DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE Tissue inhibitor of metalloproteinase TIMP.
OS Crassostrea gigas (Pacific oyster).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Periomorpha; Ostreoida;
OC Ostreoida; Ostreidae; Crassostrea.
OC NCBI_TaxID=29159;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21329024; PubMed=11434928;
RA Montagnani C., le Roux F., Berthe F., Escoubas J.M.;
RT "Cg-TIMP, an inducible tissue inhibitor of metalloproteinase from the
RT Pacific oyster Crassostrea gigas with a potential role in wound
RT healing and defense mechanisms.";
RL FEBS Lett. 500:64-70(2001).
DR ENBL: AF321279; NAG42824.1; -.
DR HSSP: Pf6035; IIR9.
DR InterPro: IPR001820; TIMP.
DR Pfam: PF00965; TIMP; 1.

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DR SMART; SMO0206; TIMP; 1.  
SQ SEQUENCE 221 AA; 25332 MW; AAS3F67EB137A06A CRC64;

Query Match 19.3%; Score 111.5; DB 5; Length 221;  
Best Local Similarity 27.5%; Pred. No. 6.7e-05;  
Matches 33; Conservative 19; Mismatches 41; Indels 27; Gaps 6;

QY 1 CTCVPPHPQTAFNSDLVIRAKFV-----GTP---EVNQTLYQRYEIKMTKMY 46  
DB 23 CMCDFTFHPNNKCSADPVIKATIVKELKFGDESMGIPFLQGNLYVQPKKDI-----F 77  
QY 47 KCPQALGDAADIRFYVTPMESVCGYFHRSHNRSEFLIAGLQDGLHITTCFVAPWN 106  
DB 78 KSSSLIG--SDPTLVIKTSGTPMNCG---ETFLINKKEYVISGFVSDGEFFTNCCQ---WN 129

## RESULT 13

Q9QV14 PRELIMINARY; PRT; 30 AA.

Q9QV14  
AC Q9QV14;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
DE Collagenase inhibitor MS-22 (Fragment).  
OS Mus sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10095;

RN [1]  
RP SEQUENCE.  
RX MEDLINE=95105266; PubMed=7806596;  
RA Rosenthal R.A., Moses M.A., Shintani Y., Megyesi J.F., Langer R.,  
RA Folkman J.;  
RT "Purification and characterization of two collagenase inhibitors from  
RT mouse sarcoma 180 conditioned medium.";  
RL J. Cell. Biochem. 56:97-105(1994).  
DR HSP; P16035; IBR9.  
DR InterPro: IPR001820; TIMP.  
DR Pfam: PF00965; TIMP; 1.  
DR PROSITE: PS00288; TIMP; 1.  
SQ SEQUENCE 30 AA; 3232 MW; EB658F1186284D9 CRC64;

Query Match 18.3%; Score 106; DB 11; Length 30;  
Best Local Similarity 63.3%; Pred. No. 2.7e-05;  
Matches 19; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

1 CTCVPPHPQTAFNSDLVIRAKFVGTPEVN 30  
1 CSQSPVHPQAFNCNADVIRAKAVSEKVD 30

## RESULT 14

Q9NDF1 PRELIMINARY; PRT; 187 AA.

Q9NDF1  
AC Q9NDF1;  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
DE Hypothetical esophageal gland cell secretory protein 12.  
GN HSP12.  
OS Heterodera glycyines (Soybean cyst nematode).  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;  
OC Tylenchoidea; Heteroderidae; Heteroderinae; Heterodera.  
OX NCBI\_TaxID=51029;

RN [1]  
RP SEQUENCE FROM N.A.  
RA Wang X., Ding X., Maier T., Goellner M., Baum T.J., Hussey R.S.,  
RA Davis E.L.;  
RT "Nematode metalloproteinase inhibitor precursor";  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF159591; AAF76926.1; -  
DR InterPro: IPR001820; TIMP.  
DR Pfam: PF00965; TIMP; 1.

DR SMART; SMO0206; TIMP; 1.  
SQ SEQUENCE 187 AA; 21450 MW; C171A2589B8824D8 CRC64;

Query Match 14.4%; Score 83.5; DB 5; Length 187;  
Best Local Similarity 23.0%; Pred. No. 0.1;  
Matches 26; Conservative 20; Mismatches 50; Indels 17; Gaps 3;

QY 1 CTCVPPHPQTAFNSDLVIRAKFVGTPE-----VNQTTLYQRYEIKMTKMYKGFQA 51  
DB 38 CCGQAPRPNDYSCSDWVAHVQIRKQGVMPAGITRQDTLNSRHEKYLARMKRISKQ 97  
QY 52 LCDADDIRF---VYTPMESVCGYFHRSHNRSEFLIAGLQDGLHITTC 99  
DB 98 MEVNOQNVILPENVYATATEDAACILLSES---GHQYLIAGDGVNAGTMTGLC 147

## RESULT 15

Q93ZH6 PRELIMINARY; PRT; 257 AA.

Q93ZH6  
AC Q93ZH6;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
DE Hypothetical protein SAV0410.  
GN SAV0410.

OS Staphylococcus aureus (strain Mu50 / ATCC 700699).  
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;  
OC Staphylococcus.  
OX NCBI\_TaxID=158878;

RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=2311952; PubMed=11418146;  
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,  
RA Cui L., Oguchi A., Aoki K., I., Nagai Y., Iian J.-Q., Ito T.,  
RA Kanemori M., Matsumaru H., Murayama A., Murakami A.,  
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,  
RA Sekimizu K., Hiraoka H., Kuhara S., Goto S., Yabuzaki J.,  
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,  
RA Hattori M., Ogasawara N., Hayashi H., Hiratake S. K.;  
RT "Whole genome sequencing of methicillin-resistant Staphylococcus  
RT aureus.";  
RL Lancet 357:1225-1240(2001).  
DR EMBL; AP003359; BAB56572.1; -  
KW Hypothetical protein; Complete proteome.

QY SEQUENCE 257 AA; 30671 MW; FEBD7041A994BEE3 CRC64;

Query Match 13.0%; Score 75.5; DB 16; Length 257;  
Best Local Similarity 28.8%; Pred. No. 1.2;  
Matches 23; Conservative 11; Mismatches 25; Indels 21; Gaps 3;

QY 8 POTAFNSDLVIRAKFVGTPEVNQTTLYQRYEIKMTKMYKGFQALG-----DAADIRF 60  
DB 66 PDSLSQTTDYLEIGKMCFLPEMNQTN-----YFQSQALSAIKMLKEHTDCHF 113  
QY 61 VYTPA--MESVCGYFHRSHN 78  
DB 114 LYTLADGIEGKCGYVQASN 133

Search completed: December 17, 2002, 15:08:10  
Job time : 20.3724 secs

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